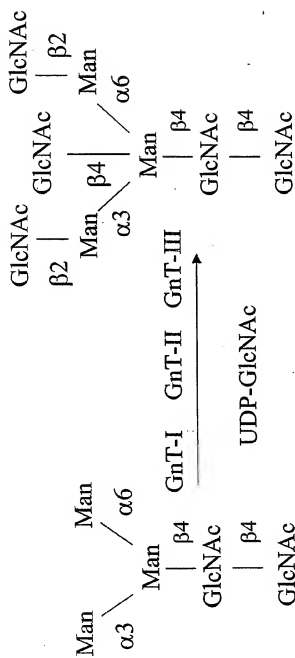


1/498



Trimannosyl core with
Bisecting GlcNAc

FIG. 1

2/498

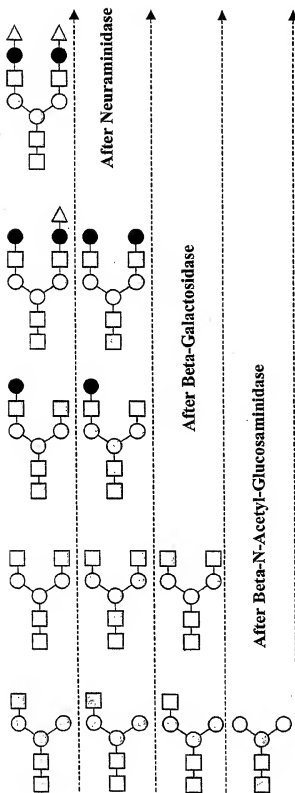
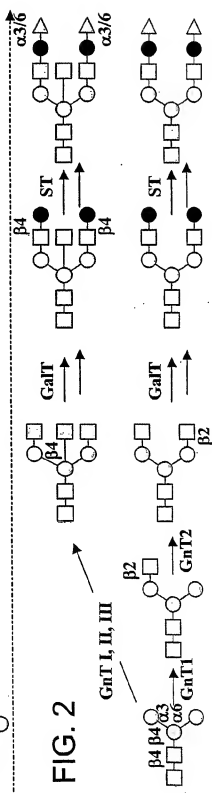


FIG. 2



3/498

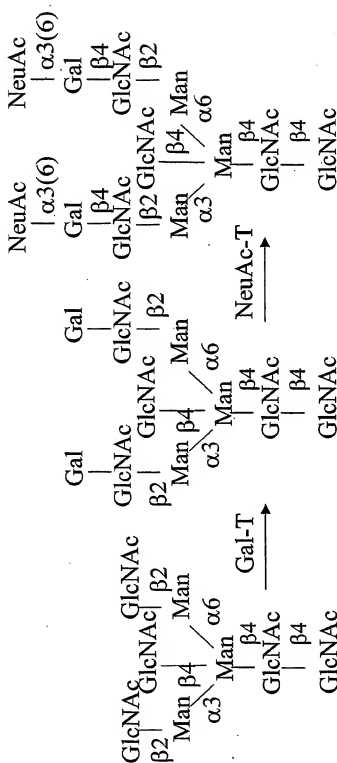


FIG. 3

5/498

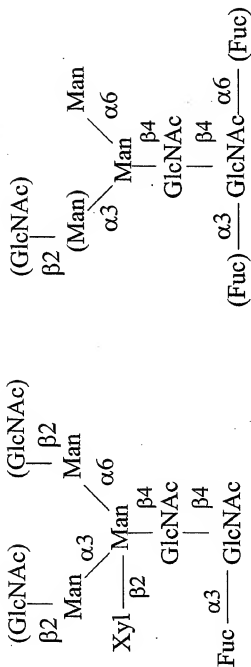


FIG. 5

FIG. 6

6/498

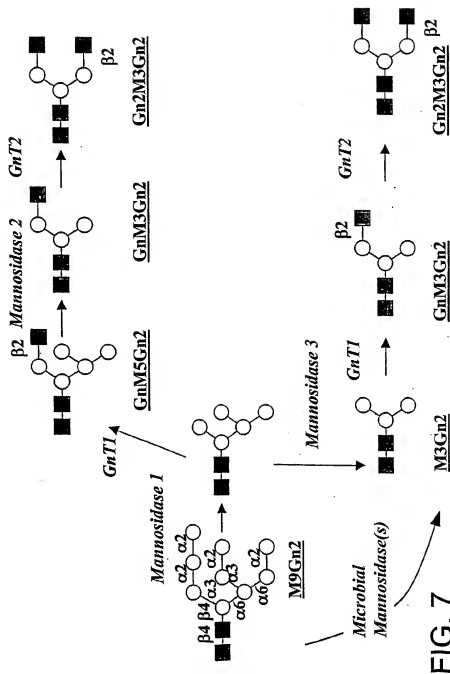


FIG. 7

7/498

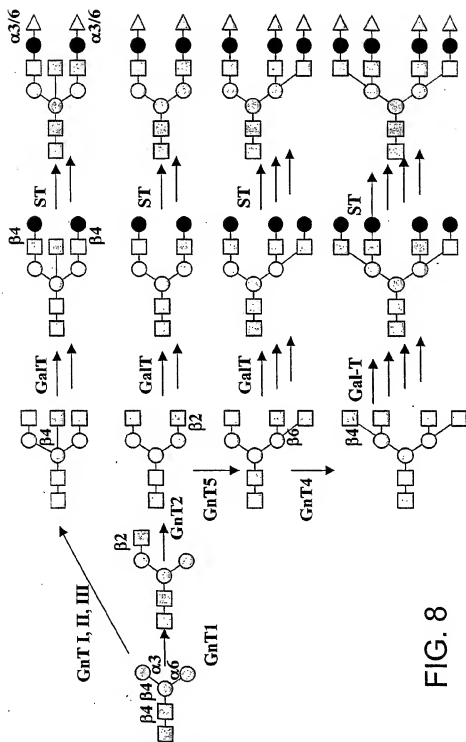


FIG. 8

8/498

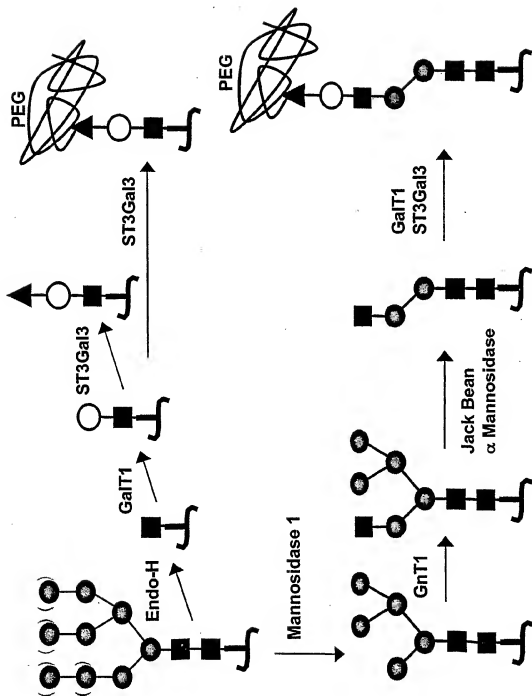
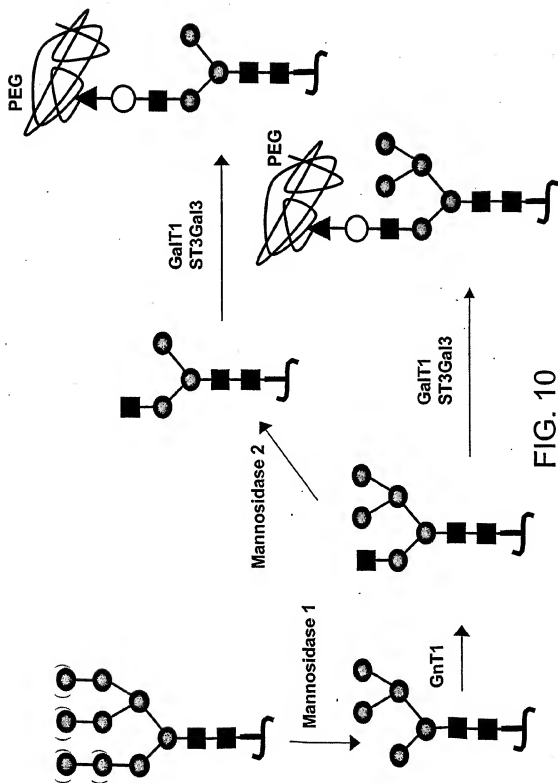


FIG. 9

9/498



10/498

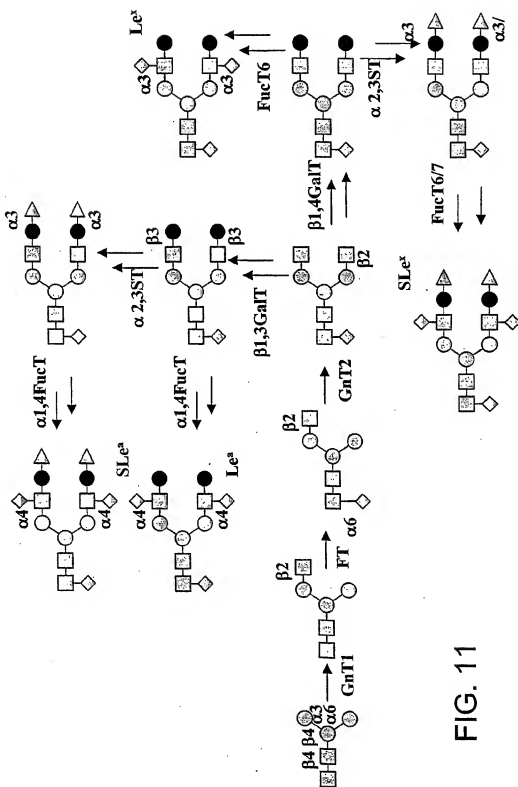


FIG. 11

11/498

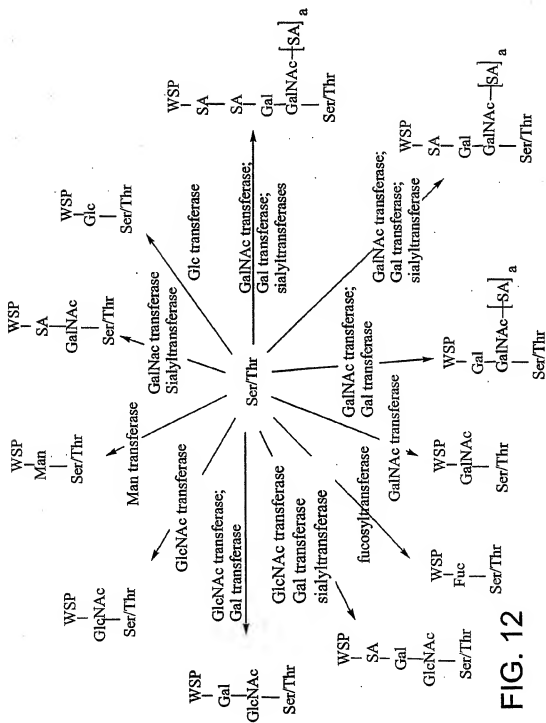


FIG. 12

12/498

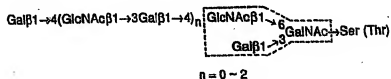
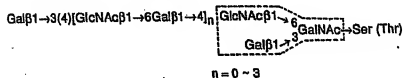
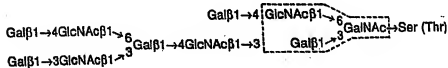
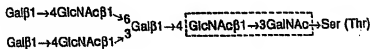
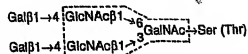
Core 1**Core 2** $n = 0 \sim 2$  $n = 0 \sim 3$ **Core 3****Core 4**

FIG. 13

14/498

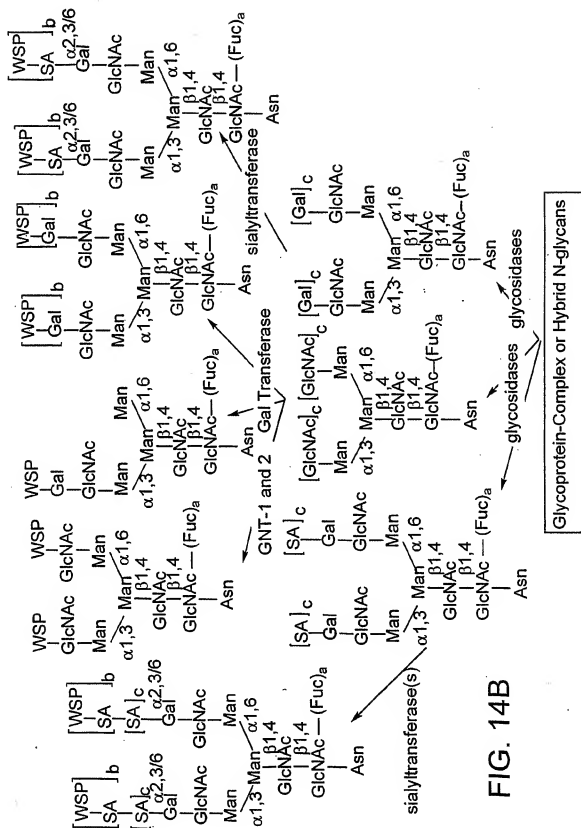


FIG. 14B

17/498

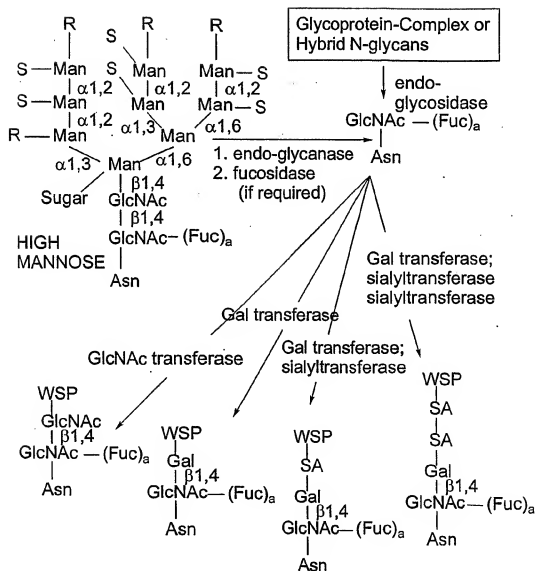


FIG. 17

22/498

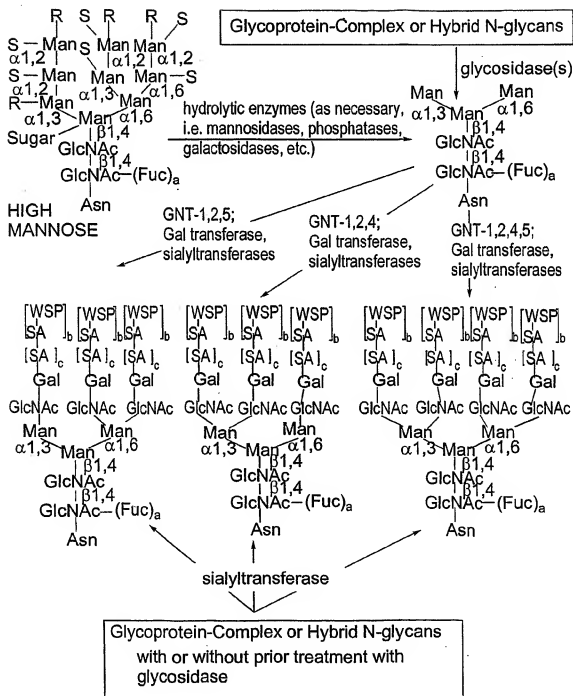


FIG. 20

25/498

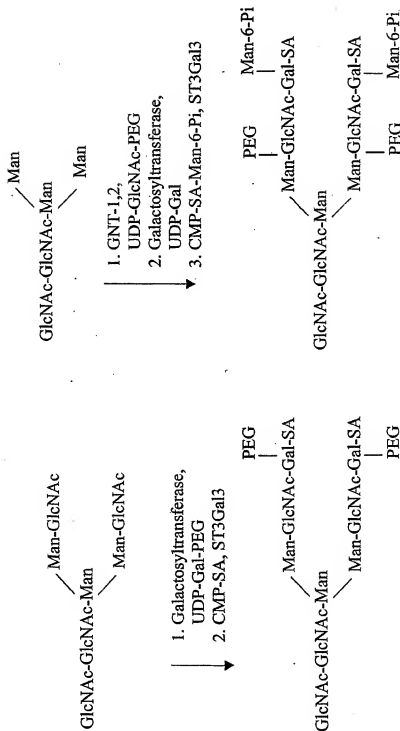


FIG. 23B

FIG. 23A

26/498

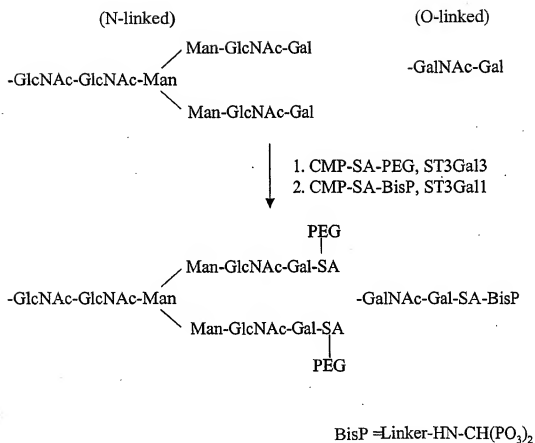


FIG. 23C

27/498

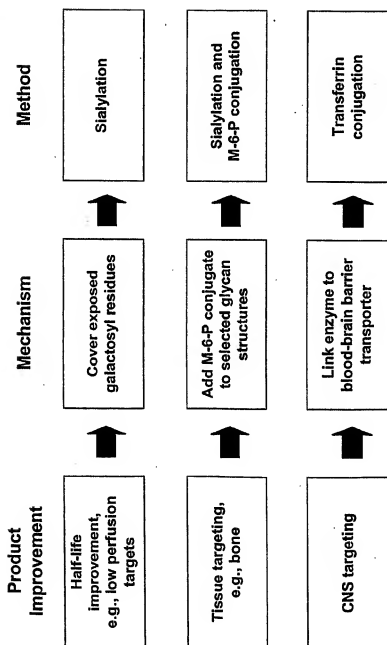


FIG. 24

28/498

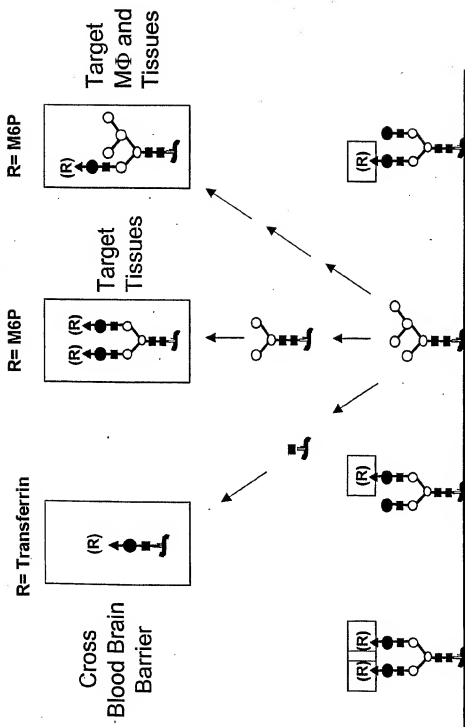


FIG. 25

29/498

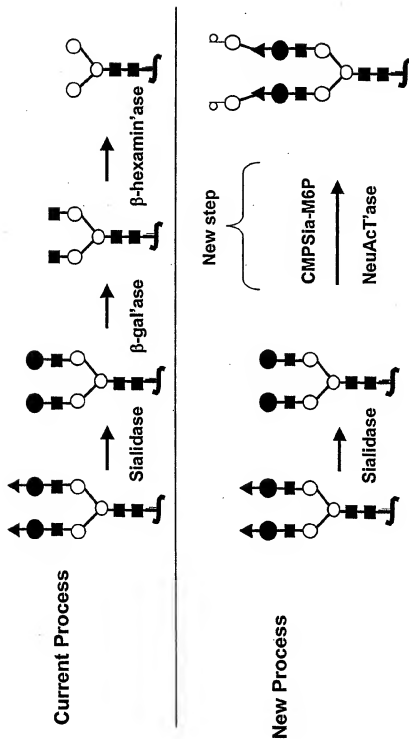


FIG. 26

30/498

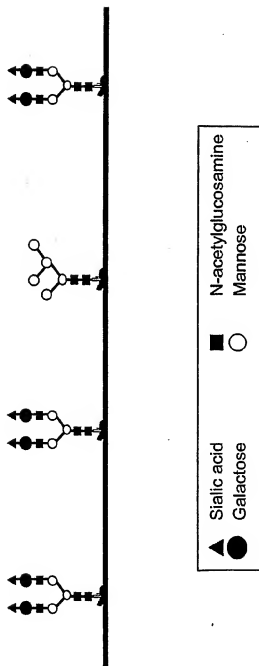


FIG. 27

31/498

12AP1/E5 -- Viventia Biotech
 1964 -- Aventis
 20K growth hormone -- AMUR
 28P6/E6 -- Viventia Biotech
 3-Hydroxyphthaloyl-beta-lactoglobulin --
 4-IBB ligand gene therapy --
 64-Cu MAb conjugate TETA-1A3 --
 Mallinckrodt Institute of Radiology
 64-Cu MAb conjugate TETA-cT84.66
 64-Cu Trastuzumab TETA conjugate --
 Genentech
 A 200 -- Amgen
 A10255 -- Eli Lilly
 A1PDX -- Hedral Therapeutics
 A6 -- Angstrom
 aaAT-III -- Genzyme
 Abciximab -- Centocor
 ABI.001 -- Atlantic BioPharmaceuticals
 ABT-828 -- Abbott
 Accutin
 Actinohivin
 activin -- Biotech Australia, Human
 Therapeutics, Curis
 AD 439 -- Tanox
 AD 519 -- Tanox
 Adalimumab -- Cambridge Antibody Tech.
 Adenocarcinoma vaccine -- Biomira -- NIS
 Adenosine deaminase -- Enzond
 Adenosine A2B receptor antagonists --
 Adenosine Therapeutics
 ADP-001 -- Axis Genetics
 AF 13948 -- Affymax
 Afelimomab -- Knoll
 AFP-SCAN -- Immunomedics
 AG 2195 -- Corixa
 agalsidase alfa -- Transkaryotic Therapies
 agalsidase beta -- Genzyme
 AGENT-- Antisoma
 AI 300 -- Autolimmune
 AI-101 -- Teva
 AI-102 -- Teva
 AI-201 -- Autolimmune
 AI-301 -- Autolimmune
 AIDS vaccine -- ANRS, CIBG, Hesed
 Biomed, Hollis-Eden, Rome, United
 Biomedical, American Home Products,
 Maxygen
 airway receptor ligand -- IC Innovations
 AJW 2 -- Ajinomoto
 AK 30 NGF -- Alkermes
 Albuferon -- Human Genome Sciences
 albumin -- Biogen, DSM Anti-Infectives,
 Genzyme Transgenics, PPL Therapeutics,
 TranXenoGen, Welfide Corp.
 aldesleukin -- Chiron
 alefacept -- Biogen
 Alemtuzumab
 Allergy therapy -- ALK-Abello/Maxygen,
 ALK-Abello/RP Scherer
 allergy vaccines -- Allergy Therapeutics
 Alnidofibatide -- Aventis Pasteur
 Alnorine -- SRC VB VECTOR
 ALP 242 -- Gruenenthal
 Alpha antitrypsin -- Arriva/Hyland
 Immuno/ProMetic/Protease Sciences
 Alpha-1 antitrypsin -- Cutter, Bayer, PPL
 Therapeutics, Profile, ZymoGenetics,
 Arriva
 Alpha-1 protease inhibitor -- Genzyme
 Transgenics, Welfide Corp.
 Alpha-galactose fusion protein --
 Immunomedics
 Alpha-galactosidase A -- Research
 Corporation Technologies, Genzyme
 Alpha-glucosidase -- Genzyme, Novazyme
 Alpha-lactalbumin
 Alpha-L-iduronidase -- Transkaryotic
 Therapies, BioMarin
 alteplase -- Genentech
 alvircept sudotox -- NIH
 ALX-0600, a GLP-2 agonist -- NPS Allelix
 Corp.

FIG. 28A

32/498

ALX1-11 --sNPS Pharmaceuticals
 Alzheimer's disease gene therapy
 AM-133 -- AMRAD
 Amb a 1 immunostim conj. -- Dynavax
 AMD 3100 -- AnorMED -- NIS
 AMD 3465 -- AnorMED -- NIS
 AMD 3465 -- AnorMED -- NIS
 AMD Fab -- Genentech
 Amediplase -- Menarini, Novartis
 AM-F9
 Amoebiasis vaccine
 Amphiregulin -- Octagene
 anakinra -- Amgen
 analgesic -- Nobex
 aneastim -- Amgen
 Anergix.RA -- Corixa, Organon
 Angiocidin -- InKine
 angiogenesis inhibitors -- ILEX
 AngioMab -- Antisoma
 Angiopoietins -- Regeneron/Procter &
 Gamble
 angiostatin -- EntreMed
 Angiostatin/endostatin gene therapy --
 Genetix Pharmaceuticals
 angiotensin-II, topical -- Maret
 Anthrax -- EluSys Therapeutics/US Army
 Medical Research Institute
 Anthrax vaccine
 Anti platelet-derived growth factor D human
 monoclonal antibodies -- CuraGen
 Anti-17-1A Mab 3622W94 --
 GlaxoSmithKline
 Anti-2C4 Mab -- Genentech
 anti-4-1BB monoclonal antibodies -- Bristol-
 Myers Squibb
 Anti-Adhesion Platform Tech. -- CytoVax
 Anti-adipocyte Mab -- Cambridge Antibody
 Tech./ObeSys
 antiallergics -- Maxygen
 antiallergy vaccine -- Acambis
 Anti-alpha-4-integrin Mab
 Anti-alphavβ3 integrin Mab -- Applied
 Molecular Evolution
 Anti-angiogenesis monoclonal antibodies --
 KS Biomedix/Schering AG
 Anti-B4 Mab-DC1 conjugate -- ImmunoGen
 Anti-B7 antibody PRIMATIZED -- IDEC
 Anti-B7-1 Mab 16-10A1
 Anti-B7-1 Mab 1G10
 Anti-B7-2 Mab GL-1
 Anti-B7-2-gelonin immunotoxin --
 Antibacterials/antifungals --
 Diversa/IntraBiotics
 Anti-beta-amyloid monoclonal antibodies --
 Cambridge Antibody Tech., Wyeth-Ayerst
 Anti-BLyS antibodies -- Cambridge
 Antibody Tech./Human Genome Sciences
 Antibody-drug conjugates -- Seattle
 Genetics/Eos
 Anti-C5 Mab BB5-1 -- Alexion
 Anti-C5 Mab N19-8 -- Alexion
 Anti-C8 Mab
 anticancer cytokines -- BioPulse
 anticancer matrix -- Telios Integra
 Anticancer monoclonal antibodies -- ARIUS,
 Immunex
 anticancer peptides -- Maxygen, Micrologix
 Anticancer prodrug Tech. -- Alexion
 Antibody Technologies
 anticancer Troy-Bodies -- Affite -- Affitech
 anticancer vaccine -- NIH
 anticancers -- Epimmune
 Anti-CCR5/CXCR4 sheep Mab -- KS
 Biomedix Holdings
 Anti-CD11a Mab KBA --
 Anti-CD11a Mab M17
 Anti-CD11a Mab TA-3 --
 Anti-CD11a Mab WT.1 --
 Anti-CD11b Mab -- Pharmacia
 Anti-CD11b Mab LM2
 Anti-CD154 Mab -- Biogen
 Anti-CD16-anti-CD30 Mab -- Biotest

FIG. 28B

33/498

Anti-CD18 MAb -- Pharmacia	Anti-CD4 MAb -- Centocor, IDEC
Anti-CD19 MAb B43 --	Pharmaceuticals, Xenova Group
Anti-CD19 MAb -liposomal sodium butyrate conjugate --	Anti-CD4 MAb 16H5
Anti-CD147	Anti-CD4 MAb 4162W94 -- GlaxoSmithKline
Anti-CD19 MAb-saporin conjugate --	Anti-CD4 MAb B-F5 -- Diaclone
Anti-CD19-dsFv-PE38-immunotoxin --	Anti-CD4 MAb GK1-5
Anti-CD2 MAb 12-15 --	Anti-CD4 MAb KT6
Anti-CD2 MAb B-E2 -- Diaclone	Anti-CD4 MAb OX38
Anti-CD2 MAb OX34 --	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb OX54 --	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX55 --	Anti-CD4 MAb W3/25
Anti-CD2 MAb RM2-1	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb RM2-2	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-4	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD20 MAb BCA B20	Anti-CD40 MAb
Anti-CD20-anti-Fc alpha RI bispecific MAb -- Medarex, Tenovus	Anti-CD40 MAb 5D12 -- Tanox
Anti-CD22 MAb-saporin-6 complex --	Anti-CD44 MAb A3D8
Anti-CD3 Immunotoxin --	Anti-CD44 MAb GKWA3
Anti-CD3 MAb 145-2C11 -- Pharming	Anti-CD44 MAb IM7
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD44 MAb KM81
Anti-CD3 MAb humanised -- Protein Design, RW Johnson	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb WT32	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb-ricin-chain-A conjugate --	Anti-CD45RB MAb
Anti-CD3 MAb-xanthine-oxidase conjugate --	Anti-CD48 MAb HuLy-m3
Anti-CD30 MAb BerH2 -- Medac	Anti-CD48 MAb WM-63
Anti-CD30 MAb-saporin conjugate	Anti-CD5 MAb -- Becton Dickinson
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD5 MAb OX19
Anti-CD38 MAb AT13/5	Anti-CD6 MAb
Anti-CD38 MAb-saporin conjugate	Anti-CD7 MAb-PAP conjugate
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb -- Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-MOV18 MAb -- Centocor	Anti-CD8 MAb OX8
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD80 MAb P16C10 -- IDEC
Anti-CD4 idiotype vaccine	Anti-CD80 MAb P7C10 -- ID Vaccine
	Anti-CD8-idarubicin conjugate
	Anti-CEA MAb CE-25
	Anti-CEA MAb MN 14 -- Immunomedics

FIG. 28C

34/498

- Anti-CEA MAb MN14-PE40 conjugate -- Immunomedics
- Anti-CEA MAb T84.66-interleukin-2 conjugate
- Anti-CEA sheep MAb -- KS Biomedix Holdings
- Anti-cell surface monoclonal antibodies -- Cambridge Antibody Tech. /Pharmacia
- Anti-c-erbB2-anti-CD3 bifunctional MAb -- Otsuka
- Anti-CMV MAb -- Scotgen
- Anti-complement
- Anti-CTLA-4 MAb
- Anti-EGFR catalytic antibody -- Hersed Biomed
- anti-EGFR immunotoxin -- IVAX
- Anti-EGFR MAb -- Abgenix
- Anti-EGFR MAb 528
- Anti-EGFR MAb KSB 107 -- KS Biomedix
- Anti-EGFR MAb-DM1 conjugate -- ImmunoGen
- Anti-EGFR MAb-LA1 --
- Anti-EGFR sheep MAb -- KS Biomedix
- Anti-FAP MAb F19-I-131
- Anti-Fas IgM MAb CH11
- Anti-Fas MAb Jo2
- Anti-Fas MAb RK-8
- Anti-Fit-1 monoclonal antibodies -- ImClone
- Anti-fungal peptides -- State University of New York
- antifungal tripeptides -- BTG
- Anti-ganglioside GD2 antibody-interleukin-2 fusion protein -- Lexigen
- Anti-GM2 MAb -- Kyowa
- Anti-GM-CSF receptor monoclonal antibodies -- AMRAD
- Anti-gp130 MAb -- Tosoh
- Anti-HCA monoclonal antibodies -- AltaRex/Epigen
- Anti-hCG antibodies -- Abgenix/AVI BioPharma
- Anti-heparanase human monoclonal antibodies -- Oxford Glycosciences/Medarex
- Anti-hepatitis C virus human monoclonal antibodies -- XTL Biopharmaceuticals
- Anti-HER-2 antibody gene therapy
- Anti-herpes antibody -- Epicyte
- Anti-HIV antibody -- Epicyte
- anti-HIV catalytic antibody -- Hersed Biomed
- anti-HIV fusion protein -- Idun
- anti-HIV proteins -- Cangene
- Anti-HM1-24 MAb -- Chugai
- Anti-hrR3 MAb
- Anti-Human-Carcinoma-Antigen MAb -- Epicyte
- Anti-ICAM-1 MAb -- Boehringer Ingelheim
- Anti-ICAM-1 MAb 1A-29 -- Pharmacia
- Anti-ICAM-1 MAb HA58
- Anti-ICAM-1 MAb YN1/1.7.4
- Anti-ICAM-3 MAb ICM3 -- ICOS
- Anti-idiotypic breast cancer vaccine 11D10
- Anti-idiotypic breast cancer vaccine ACA14C5 --
- Anti-idiotypic cancer vaccine -- ImClone Systems/Merck KGaA ImClone, Viventia Biotech
- Anti-idiotypic cancer vaccine 1A7 -- Titan
- Anti-idiotypic cancer vaccine 3H1 -- Titan
- Anti-idiotypic cancer vaccine TriAb -- Titan
- Anti-idiotypic Chlamydia trachomatis vaccine
- Anti-idiotypic colorectal cancer vaccine -- Novartis
- Anti-idiotypic colorectal cancer vaccine -- Onyvox
- Anti-idiotypic melanoma vaccine -- IDEC Pharmaceuticals
- Anti-idiotypic ovarian cancer vaccine ACA 125
- Anti-idiotypic ovarian cancer vaccine AR54 - AltaRex

FIG. 28D

35/498

Anti-idiotype ovarian cancer vaccine CA-125 – AltaRex, Biomira	Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University
Anti-IgE catalytic antibody -- Hesed Biomed	Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital
Anti-IgE MAb E26 -- Genentech	Anti-MHC monoclonal antibodies
Anti-IGF-1 MAb	Anti-MIF antibody humanised -- IDEC, Cytokine PharmaSciences
anti-inflammatory -- GeneMax	Anti-MRSA/VRSA sheep MAb -- KS Biomedix Holdings
anti-inflammatory peptide -- BTG	Anti-mu MAb -- Novartis
anti-integrin peptides -- Burnha	Anti-MUC-1 MAb
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC 18
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb IN1
Anti-interferon-gamma polyclonal antibody - Advanced Biotherapy	Anti-nuclear autoantibodies -- Procyon
Anti-interleukin-10 MAb --	Anti-ovarian cancer monoclonal antibodies -
Anti-interleukin-12 MAb --	- Dompe
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Anti-p185 monoclonal antibodies
Anti-interleukin-2 receptor MAb 2A3	Anti-p43 MAb
Anti-interleukin-2 receptor MAb 33B3-1 -- Immunotech	Antiparasitic vaccines
Anti-interleukin-2 receptor MAb ART-18	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAb LO-Tact-1	Anti-properdin monoclonal antibodies -- Abgenix/Gliatech
Anti-interleukin-2 receptor MAb Mikbeta1	Anti-PSMA (prostrate specific membrane antigen)
Anti-interleukin-2 receptor MAb NDS61	Anti-PSMA MAb J591 -- BZL Biologics
Anti-interleukin-4 MAb 11B11	Anti-Rev MAb gene therapy --
Anti-interleukin-5 MAb -- Wallace Laboratories	Anti-RSV antibodies -- Epicyte, Intracell
Anti-interleukin-6 MAb -- Centocor, Diacorne, Pharmadigm	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-8 MAb -- Abgenix	Anti-RSV MAb, inhalation -- Alkermes/MedImmune
Anti-interleukin-8 MAb -- Xenotech	Anti-RT gene therapy
Anti-JL1 MAb	Antisense K-ras RNA gene therapy
Anti-Klebsiella sheep MAb -- KS Biomedix Holdings	Anti-SF-25 MAb
Anti-Laminin receptor MAb-liposomal doxorubicin conjugate	Anti-sperm antibody -- Epicyte
Anti-LCG MAb -- Cytoclonal	Anti-Tac(Fv)-PE38 conjugate
Anti-lipopolysaccharide MAb -- VitaResc	Anti-TAPA/CD81 MAb AMP1
	Anti-tat gene therapy

FIG. 28E

36/498

Anti-TCR-alphabeta MAb H57-597
 Anti-TCR-alphabeta MAb R73
 Anti-tenascin MAb BC-4-I-131
 Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme
 Anti-TGF-beta MAb 2G7 -- Genentech
 Antithrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad
 Anti-Thy1 MAb
 Anti-Thy1.1 MAb
 Anti-tissue factor/factor VIIA sheep MAb -- KS Biomedix
 Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharacia, Sero
 Anti-TNF sheep MAb -- KS Biomedix Holdings
 Anti-TNFalpha MAb -- Genzyme
 Anti-TNFalpha MAb B-C7 -- Diaclone
 Anti-tooth decay MAb -- Planet BioTech.
 Anti-TRAIL receptor-1 MAb -- Takeda
 Antitumour RNases -- NIH
 Anti-VCAM MAb 2A2 -- Alexion
 Anti-VCAM MAb 3F4 -- Alexion
 Anti-VCAM-1 MAb
 Anti-VEC MAb -- ImClone
 Anti-VEGF MAb -- Genentech
 Anti-VEGF MAb 2C3
 Anti-VEGF sheep MAb -- KS Biomedix Holdings
 Anti-VLA-4 MAb HP1/2 -- Biogen
 Anti-VLA-4 MAb PS/2
 Anti-VLA-4 MAb R1-2
 Anti-VLA-4 MAb TA-2
 Anti-VAP-1 human MAb
 Anti-VRE sheep MAb -- KS Biomedix Holdings
 ANUP -- TranXenoGen
 ANUP-1 -- Pharis
 AOP-RANTES -- Senetek
 Apan-CH -- Praecis Pharmaceuticals
 APC-8024 -- Demegen
 ApoA-1 -- Milano, Pharmacia
 Apogen -- Alexion
 apolipoprotein A1 -- Avanir
 Apolipoprotein E -- Bio-Tech. General
 Applaggin -- Biogen
 aprotinin -- ProdiGene
 APT-070C -- AdProTech
 AR 177 -- Aronex Pharmaceuticals
 AR 209 -- Aronex Pharmaceuticals, Antigenics
 AR545C
 ARGENT gene delivery systems -- ARIAD
 Arresten
 ART-123 -- Asahi Kasei
 arylsulfatase B -- BioMarin
 Arylsulfatase B, Recombinant human -- BioMarin
 AS 1051 -- Ajinomoto
 ASI-BCL -- Intracell
 Asparaginase - Merck
 ATL-101 -- Alizyme
 Atrial natriuretic peptide -- Pharis
 Aurintricarboxylic acid-high molecular weight
 Autoimmune disorders -- GPC
 Biotech/MorphoSys
 Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme
 Tra
 Autoimmune disorders/cancer -- Abgenix/Chiron, CuraGen
 Autotaxin
 Avicidin -- NeoRx
 axogenesis factor-1 -- Boston Life Sciences
 Axokine -- Regeneron
 B cell lymphoma vaccine -- Biomira
 B7-1 gene therapy --
 BABS proteins -- Chiron

FIG. 28F

37/498

BAM-002 -- Novelos Therapeutics
 Basiliximab (anti CD25 MAb) -- Novartis
 Bay-16-9996 -- Bayer
 Bay-39-9437 -- Bayer
 Bay-50-4798 -- Bayer
 BB-10153 -- British Biotech
 BBT-001 -- Bolder BioTech.
 BBT-002 -- Bolder BioTech.
 BBT-003 -- Bolder BioTech.
 BBT-004 -- Bolder BioTech.
 BBT-005 -- Bolder BioTech.
 BBT-006 -- Bolder BioTech.
 BBT-007 -- Bolder BioTech.
 BCH-2763 -- Shire
 BCSF -- Millenium Biologix
 BDNF -- Regeneron -- Amgen
 Becapiermin -- Johnson & Johnson, Chiron
 Bectumomab -- Immunomedics
 Beriplast -- Aventis
 Beta-adrenergic receptor gene therapy --
 University of Arkansas
 bFGF -- Scios
 BI 51013 -- Behringwerke AG
 BIBH 1 -- Boehringer Ingelheim
 BIM-23190 -- Beaufour-Ipsen
 birch pollen immunotherapy -- Pharmacia
 bispecific fusion proteins -- NIH
 Bispecific MAb 2B1 -- Chiron
 Bitistatin
 BIWA 4 -- Boehringer Ingelheim
 blood substitute -- Northfield, Baxter Intl.
 BLP-25 -- Biomira
 BLS-0597 -- Boston Life Sciences
 BLyS -- Human Genome Sciences
 BLyS radiolabelled -- Human Genome
 Sciences
 BM 06021 -- Boehringer Mannheim
 BM-202 -- BioMarin
 BM-301 -- BioMarin
 BM-301 -- BioMarin
 BM-302 -- BioMarin
 BMP 2 -- Genetics Institute/Medtronic-
 Sofamor Danek, Genetics Institute/
 Collagenesis, Genetics
 Institute/Yamanouch
 BMP 2 gene therapy
 BMP 52 -- Aventis Pasteur, Biopharm
 BMP-2 -- Genetics Institute
 BMS 182248 -- Bristol-Myers Squibb
 BMS 202448 -- Bristol-Myers Squibb
 bone growth factors -- IsoTis
 BPC-15 -- Pfizer
 brain natriuretic peptide --
 Breast cancer -- Oxford
 GlycoSciences/Medarex
 Breast cancer vaccine -- Therion Biologics,
 Oregon
 BSSL -- PPL Therapeutics
 BST-2001 -- BioStratum
 BST-3002 -- BioStratum
 BTI 322 --
 butyrylcholinesterase -- Shire
 C 6822 -- COR Therapeutics
 C1 esterase inhibitor -- Pharming
 C3d adjuvant -- AdProTech
 CAB-2.1 -- Millennium
 calcitonin -- Inhale Therapeutics Systems,
 Aventis, Genetronics, TranXenoGen,
 Unigene, Rhone Poulenc Rohrer
 calcitonin -- oral -- Nobex, Emisphere,
 Pharmaceutical Discovery
 Calcitonin gene-related peptide -- Asahi
 Kasei -- Unigene
 calcitonin, human -- Suntory
 calcitonin, nasal -- Novartis, Unigene
 calcitonin, Panoderm -- Elan
 calcitonin, Peptitrol -- Shire
 calcitonin, salmon -- Therapicon
 calin -- Biopharm
 Calphobindin I
 calphobindin I -- Kowa
 calreticulin -- NYU

FIG. 28G

38/498

Campath-1G
 Campath-1M
 cancer therapy -- Cangene
 cancer vaccine -- Aixlie, Aventis Pasteur,
 Center of Molecular Immunology, YM
 BioSciences, Cytos, Genzyme,
 Transgenics, GlobelImmune, Igeneon,
 ImClone, Virogenetics, InterCell, Iomai,
 Jenner Biotherapies, Memorial Sloan-
 Kettering Cancer Center, Sydney Kimmel
 Cancer Center, Novavax, Protein
 Sciences, Argonex, SIGA
 Cancer vaccine ALVAC-CEA B7.1 --
 Aventis Pasteur/Therion Biologics
 Cancer vaccine CEA-TRICOM -- Aventis
 Pasteur/Therion Biologics
 Cancer vaccine gene therapy -- Cantab
 Pharmaceuticals
 Cancer vaccine HER-2/neu -- Corixa
 Cancer vaccine THERATOPE -- Biomira
 cancer vaccine, PolyMASC -- Valentis
 Candida vaccine -- Corixa, Inhibitex
 Canstatin -- ILEX
 CAP-18 -- Panorama
 Cardiovascular gene therapy -- Collateral
 Therapeutics
 carperitide -- Suntory
 Casocidin-1 -- Pharis
 CAT 152 -- Cambridge Antibody Tech.
 CAT 192 -- Cambridge Antibody Tech.
 CAT 213 -- Cambridge Antibody Tech.
 Catalase-- Enzon
 Cat-PAD -- Circassia
 CB 0006 -- Celltech
 CCK(27-32)-- Akzo Nobel
 CCR2-64I -- NIH
 CD, Procept -- Paligent
 CD154 gene therapy
 CD39 -- Immunex
 CD39-L2 -- Hyseq
 CD39-L4 -- Hyseq
 CD4 fusion toxin -- Senetek
 CD4 IgG -- Genentech
 CD4 receptor antagonists --
 Pharmacocepeia/Progenics
 CD4 soluble -- Progenics
 CD4, soluble -- Genzyme Transgenics
 CD40 ligand -- Immunex
 CD4-ricin chain A -- Genentech
 CD59 gene therapy -- Alexion
 CD8 TIL cell therapy -- Aventis Pasteur
 CD8, soluble -- Avidex
 CD95 ligand -- Roche
 CDP 571 -- Celltech
 CDP 850 -- Celltech
 CDP-860 (PEG-PDGF MAb) -- Celltech
 CDP 870 -- Celltech
 CDS-1 -- Ernest Orlando
 Cedelizumab -- Ortho-McNeil
 Cetermin -- Insmid
 CETP vaccine -- Avant
 Cetorelix
 Cetuximab
 CGH 400 -- Novartis
 CGP 42934 -- Novartis
 CGP 51901 -- Tanox
 CGRP -- Unigene
 CGS 27913 -- Novartis
 CGS 32359 -- Novartis
 Chagas disease vaccine -- Corixa
 chemokines -- Immune Response
 CHH 380 -- Novartis
 chitinase -- Genzyme, ICOS
 Chlamydia pneumoniae vaccine -- Antex
 Biologics
 Chlamydia trachomatis vaccine -- Antex
 Biologics
 Chlamydia vaccine -- GlaxoSmithKline
 Cholera vaccine CVD 103-HgR -- Swiss
 Serum and Vaccine Institute Berne
 Cholera vaccine CVD 112 -- Swiss Serum
 and Vaccine Institute Berne

FIG. 28H

39/498

Cholera vaccine inactivated oral -- SBL	CRL 1605 -- CytRx
Vaccin	CS-560 -- Sankyo
Chrysalin -- Chrysalis BioTech.	CSF -- ZymoGenetics
CI-782 -- Hitachi Kase	CSF-G -- Hangzhou, Dong-A, Hanmi
Ciliary neurotrophic factor -- Fidia, Roche	CSF-GM -- Cangene, Hunan, LG Chem
CIM project -- Active Biotech	CSF-M -- Zarix
CL 329753 -- Wyeth-Ayerst	CT 1579 -- Merck Frosst
CL22, Cobra -- ML Laboratories	CT 1786 -- Merck Frosst
Clenoliximab -- IDEC	CT-112 ^A -- BTG
Clostridium difficile antibodies -- Epicycle	CTB-134L -- Xenova
clotting factors -- Octagene	CTC-111 -- Kaketsuken
CMB 401 -- Celltech	CTGF -- FibroGen
CNTF -- Sigma-Tau	CTLA4-Ig -- Bristol-Myers Squibb
Cocaine abuse vaccine -- Cantab,	CTLA4-Ig gene therapy --
ImmuLogic, Scripps	CTP-37 -- AVI BioPharma
coccidiomycosis vaccine -- Arizo	C-type natriuretic peptide -- Suntory
collagen -- Type I -- Pharming	CVS 995 -- Corvas Intl.
Collagen formation inhibitors -- FibroGen	CX 397 -- Nikko Kyodo
Collagen/hydroxyapatite/bone growth factor	CY 1747 -- Epimmune
-- Aventis Pasteur, Biopharm, Orquest	CY 1748 -- Epimmune
collagenase -- BioSpecifics	Cyanovirin-N
Colorectal cancer vaccine -- Wistar Institute	Cystic fibrosis therapy -- CBR/IVAX
Component B, Recombinant -- Sero	CYT 351
Connective tissue growth factor inhibitors --	cytokine Traps -- Regeneron
FibroGen/Taisho	cytokines -- Enzon, Cytodonal
Contortostat	Cytomegalovirus glycoprotein vaccine --
contraceptive vaccine -- Zonagen	Chiron, Aquila Biopharmaceuticals,
Contraceptive vaccine hCG	Aventis Pasteur, Virogenetics
Contraceptive vaccine male reversible --	Cytomegalovirus vaccine live -- Aventis
IMMUCON	Pasteur
Contraceptive vaccine zona pellucida --	Cytosine deaminase gene therapy --
Zonagen	GlaxoSmithKline
Copper-64 labelled Mab TETA-1A3 -- NCI	DA-3003 -- Dong-A
Coralyne	DAB389interleukin-6 -- Senetek
Corsevin M	DAB389interleukin-7
C-peptide analogues -- Schwarz	DAC:GLP-2 -- ConjuChem, Inc.
CPI-1500 -- Consensus	Daclizumab (anti-IL2R Mab) -- Protein
CRF -- Neurobiological Tech.	Design Labs
cRGDfV pentapeptide --	DAMP ^A -- Incyte Genomics
CRL 1095 -- CytRx	Daniplestim -- Pharmacia
CRL 1336 -- CytRx	darbepoetin alfa -- Amgen

40/498

DBI-3019 -- Diabetogen
 DCC -- Genzyme
 DDF -- Hyseq
 decorin -- Integra, Telios
 defensins -- Large Scale Biology
 DEGR-VIIa
 Delimmunised antibody 3B6/22 AGEN
 Deimmunised anti-cancer antibodies --
 Biovation/Viragen
 Dendroamide A
 Dengue vaccine -- Bavarian Nordic, Merck
 denileukin diftotox -- Ligand
 DES-1101 -- Desmos
 desirudin -- Novartis
 desmopressin -- Unigene
 Desmoteplase -- Merck, Schering AG
 Destablase
 Diabetes gene therapy -- DeveloGen, Pfizer
 Diabetes therapy -- Crucell
 Diabetes type 1 vaccine -- Diamyd
 Therapeutics
 DiaCIM -- YM BioSciences
 dialytic oligopeptides -- Research Corp
 Diamyd -- Diamyd Therapeutics
 DiaPep227 -- Peppen
 DiavaX -- Corixa
 Digoxin MAb -- Glaxo
 Diphtheria tetanus pertussis-hepatitis B
 vaccine -- GlaxoSmithKline
 DIR therapy -- Solis Therapeutics --
 DNase -- Genentech
 Dornase alfa -- Genentech
 Dornase alfa, inhalation -- Genentech
 Doxorubicin-anti-CEA MAb conjugate --
 Immunomedics
 DP-107 -- Trimeris
 drotrecogin alfa -- Eli Lilly
 DTctGMCSF
 DTP-polio vaccine -- Aventis Pasteur
 DU 257-KM231 antibody conjugate --
 Kyowa
 dural graft matrix -- Integra
 Duteplase -- Baxter Intl.
 DWP-401 -- Daewoong
 DWP-404 -- Daewoong
 DWP-408 -- Daewoong
 Dx 88 (Epi-KAL2) -- Dyax
 Dx 890 (elastin inhibitors) -- Dyax
 E coli O157 vaccine -- NIH
 E21-R -- BresaGen
 Eastern equine encephalitis virus vaccine --
 Echicetin --
 Echinhibin 1 --
 Echistatin -- Merck
 Echitamine --
 Ecromeximab -- Kyowa Hakko
 EC-SOD -- PPL Therapeutics
 Eculizumab (5G1.1) -- Alexion
 EDF -- Ajinomoto
 EDN derivative -- NIH
 EDNA -- NIH
 Edobacomab -- XOMA
 Edrecolomab -- Centocor
 EF 5077
 Efalizumab -- Genentech
 EGF fusion toxin -- Seragen, Ligand
 EGF-P64k vaccine -- Center of Molecular
 Immunology
 EL 246 -- LigoCyte
 elastase inhibitor -- Synergen
 elcatonin -- Therapicon
 EMD 72000 -- Merck KGaA
 Emdogain -- BIORA
 emfilermin -- AMRAD
 Emoctakin -- Novartis
 enamel matrix protein -- BIORA
 Endo III -- NYU
 endostatin -- EntreMed, Pharis
 Enhancins -- Micrologix
 Enlimomab -- Isis Pharm.
 Enoxaparin sodium -- Phamuka

FIG. 28J

41/498

enzyme linked antibody nutrient depletion
 therapy -- KS Biomedix Holdings
 Eosinophil-derived neutralizing agent --
 EP-51216 -- Asta Medica
 EP-51389 -- Asta Medica
 EPH family ligands -- Regeneron
 Epidermal growth factor -- Hitachi Kasei,
 Johnson & Johnson
 Epidermal growth factor fusion toxin --
 Senetek
 Epidermal growth factor-genistein --
 EPI-HNE-4 -- Dyax
 EPI-KAL2 -- Dyax
 Epoetin-alfa -- Amgen, Dragon
 Pharmaceuticals, Nanjing Huaxin
 Epratuzumab -- Immunomedics
 Epstein-Barr virus vaccine --
 Aviron/SmithKline Beecham, Bioresearch
 Eptacog alfa -- Novo Nordisk
 Eptifibatide -- COR Therapeutics
 erb-38 --
 Erlizumab -- Genentech
 erythropoietin -- Alkermes, ProLease, Dong-
 A, Elanex, Genetics Institute, LG Chem,
 Protein Sciences, Serono, Snow Brand,
 SRC VB VECTOR, Transkaryotic
 Therapies
 Erythropoietin Beta -- Hoffman La Roche
 Erythropoietin/Epoetin alfa -- Chugai
 Escherichia coli vaccine -- North American
 Vaccine, SBL Vaccin, Swiss Serum and
 Vaccine Institute Berne
 etanercept -- Immunex
 examorelin -- Mediolanum
 Exendin 4 -- Amylin
 exonuclease VII
 F 105 -- Centocor
 F-992 -- Fornix
 Factor IX -- Alpha Therapeutics, Welfide
 Corp., CSL, enetics Institute/AHP,
 Pharmacia, PPL Therapeutics
 Factor IX gene therapy -- Cell Genesys
 Factor VII -- Novo Nordisk, Bayer, Baxter
 Intl.
 Factor VIIa -- PPL Therapeutics,
 ZymoGenetics
 Factor VIII -- Bayer Genentech, Beaufour-
 Ipsen, CLB, Inex, Octagen, Pharmacia,
 Pharming
 Factor VIII -- PEGylated -- Bayer
 Factor VIII fragments -- Pharmacia
 Factor VIII gene therapy -- Targeted
 Genetics
 Factor VIII sucrose formulation -- Bayer,
 Genentech
 Factor VIII-2 -- Bayer
 Factor VIII-3 -- Bayer
 Factor Xa inhibitors -- Merck, Novo Nordisk,
 Mochida
 Factor XIII -- ZymoGenetics
 Factors VIII and IX gene therapy -- Genetics
 Institute/Targeted Genetics
 Famoxin -- Genset
 Fas (delta) TM protein -- LXR BioTech.
 Fas TR -- Human Genome Sciences
 Felvizumab -- Scotgen
 FFR-VIIa -- Novo Nordisk
 FG-001 -- F-Gene
 FG-002 -- F-Gene
 FG-004 -- F-Gene
 FG-005 -- F-Gene
 FGF + fibrin -- Repair
 Fibrimage -- Bio-Tech. General
 fibrin-binding peptides -- ISIS Innovation
 fibrinogen -- PPL Therapeutics, Pharming
 fibroblast growth factor -- Chiron, NYU,
 Ramot, ZymoGenetics
 fibrolase conjugate -- Schering AG
 Filgrastim -- Amgen
 filgrastim -- PDA modified -- Xencor
 FLT-3 ligand -- Immunex
 FN18 CRM9 --

FIG. 28K

42/498

follostatin -- Biotech Australia, Human Therapeutics	Glucocerebrosidase -- Genzyme
folliotropin alfa -- Alkermes, ProLease, PowderJect, Sero, Akzo Nobel	glutamate decarboxylase -- Genzyme Transgenics
Follitropin Beta -- Bayer, Organon	Glycoprotein S3 -- Kureha
FP 59	GM-CSF -- Immunhex
FSH -- Ferring	GM-CSF tumour vaccine -- PowderJect
FSH + LH -- Ferring	GnRH immunotherapeutic -- Protherics
F-spondin -- CeNeS	Goserelin (LhRH antagonist) -- AstraZeneca
fusion protein delivery system -- UAB Research Foundation	gp75 antigen -- ImClone
fusion toxins -- Boston Life Sciences	gp96 -- Antigenics
G 5598 -- Genentech	GPI 0100 -- Galenica
GA-II -- Transkaryotic Therapies	GR 4991W93 -- GlaxoSmithKline
Gamma-interferon analogues -- SRC VB VECTOR	Granulocyte colony-stimulating factor -- Dong-A
Ganirelix -- Roche	Granulocyte colony-stimulating factor conjugate
gastric lipase -- Meristem	grass allergy therapy -- Dynavax
Gavilimomab --	GRF1-44 -- ICN
G-CSF -- Amgen, SRC VB VECTOR	Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo
GDF-1 -- CeNeS	growth factor peptides -- Biotherapeutics
GDF-5 -- Biopharm	growth hormone -- LG Chem
GDNF (glial derived neurotrophic factor) -- Amgen	growth hormone, Recombinant human -- Sero
gelsolin -- Biogen	GT 4086 -- Gliatech
Gemtuzumab ozogamicin -- Celltech	GW 353430 -- GlaxoSmithKline
Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies	GW-278884 -- GlaxoSmithKline
Glanzmann thrombasthenia gene therapy --	H 11 -- Viventia Biotech
Glatiramer acetate -- Yeda	H5N1 influenza A virus vaccine -- Protein Sciences
glial growth factor 2 -- CeNeS	haemoglobin -- Biopure
GLP-1 -- Amylin, Suntory, TheraTech, Watson	haemoglobin 3011, Recombinant -- Baxter Healthcare
GLP-1 peptide analogues -- Zealand Pharmaceuticals	haemoglobin crosfumaryl -- Baxter Intl.
GLP-2 -- Novo Nordisk, Ontario, Inc., Suntory Limited	haemoglobin stabilized -- Ajinomoto
glucagon -- Eli Lilly, ZymoGenetics	haemoglobin, recombinant -- Apex
Glucagon-like peptide-1 7-36 amide -- Suntory	HAF -- Immune Response
Glucogen-like peptide -- Amylin	Hantavirus vaccine
	HB 19
	HBNF -- Regeneron
	HCC-1 -- Pharis

FIG. 28L

43/498

hCG -- Milkhaus
 hCG vaccine -- Zonagen
 HE-317 -- Hollis-Eden Pharmaceuticals
 Heat shock protein cancer and influenza
 vaccines -- StressGen
 Helicobacter pylori vaccine -- Acambis,
 AstraZeneca/CSL, Chiron, Provalis
 Helistat-G -- GalaGen
 Hemolink -- Hemosol
 hepapoietin -- Snow Brand
 heparanase -- InSight
 heparinase I -- Ibex
 heparinase III -- Ibex
 Hepatitis A vaccine -- American Biogenetic
 Sciences
 Hepatitis A vaccine inactivated
 Hepatitis A vaccine Nothav -- Chiron
 Hepatitis A-hepatitis B vaccine --
 GlaxoSmithKline
 hepatitis B therapy -- Tripep
 Hepatitis B vaccine -- Amgen, Chiron SpA,
 Meiji Milk, NIS, Prodeva, PowderJect,
 Rhein Biotech
 Hepatitis B vaccine recombinant -- Evans
 Vaccines, Epitex Combiotech, Genentech,
 MedImmune, Merck Sharp & Dohme,
 Rhein Biotech, Shantha Biotechnics,
 Vector, Yeda
 Hepatitis B vaccine recombinant TGP 943 --
 Takeda
 Hepatitis C vaccine -- Bavarian Nordic,
 Chiron, Innogenetics Acambis,
 Hepatitis D vaccine -- Chiron Vaccines
 Hepatitis E vaccine recombinant --
 Genelabs/GlaxoSmithKline, Novavax
 hepatocyte growth factor -- Panorama,
 Sosei
 hepatocyte growth factor kringle fragments -
 - EntreMed
 Her-2/Neu peptides -- Corixa
 Herpes simplex glycoprotein DNA vaccine --
 Merck, Wyeth-Lederle Vaccines-Malvern,
 Genentech, GlaxoSmithKline, Chiron,
 Takeda
 Herpes simplex vaccine -- Cantab
 Pharmaceuticals, CEL-SCI, Henderson
 Morley
 Herpes simplex vaccine live -- ImClone
 Systems/Wyeth-Lederle, Aventis Pasteur
 HGF derivatives -- Dompe
 hAPP vaccine -- Crucell
 Hib-hepatitis B vaccine -- Aventis Pasteur
 HIC 1
 HIP-- Altachem
 Hirudins -- Biopharma, Cangene, Dongkook,
 Japan Energy Corporation, Pharmacia
 Corporation, SIR International, Sanofi-
 Synthelabo, Sotragene, Rhein Biotech
 HIV edible vaccine -- ProdiGene
 HIV gp120 vaccine -- Chiron, Ajinomoto,
 GlaxoSmithKline, ID Vaccine, Progenics,
 VaxGen
 HIV gp120 vaccine gene therapy --
 HIV gp160 DNA vaccine -- PowderJect,
 Aventis Pasteur, Oncogen, Hyland
 Immuno, Protein Sciences
 HIV gp41 vaccine -- Panacos
 HIV HGP-30W vaccine -- CEL-SCI
 HIV immune globulin -- Abbott, Chiron
 HIV peptides -- American Home Products
 HIV vaccine -- Applied bioTech., Axis
 Genetics, Biogen, Bristol-Myers Squibb,
 Genentech, Korea Green Cross, NIS,
 Oncogen, Protein Sciences Corporation,
 Terumo, Tonen Corporation, Wyeth-
 Ayerst, Wyeth-Lederle Vaccines-Malvern,
 Advanced BioScience Laboratories,
 Bavarian Nordic, Bavarian Nordic/Statens
 Serum Institute, GeneCure, Immune
 Response, Progenics, Theron Biologics,
 United Biomedical, Chiron

FIG. 28M

44/498

HIV vaccine vCP1433 -- Aventis Pasteur
 HIV vaccine vCP1452 -- Aventis Pasteur
 HIV vaccine vCP205 -- Aventis Pasteur
 HL-9 -- American BioScience
 HM-9239 -- Cytran
 HML-103 -- Hemosol
 HML-104 -- Hemosol
 HML-105 -- Hemosol
 HML-109 -- Hemosol
 HML-110 -- Hemosol
 HML-121 -- Hemosol
 hNLP -- Pharis
 Hookworm vaccine
 host-vector vaccines -- Henogen
 HPM 1 -- Chugai
 HPV vaccine -- MediGene
 HSA -- Meristem
 HSF -- StressGen
 HSP carriers -- Weizmann, Yeda, Peptor
 HSPPC-70 -- Antigenics
 HSPPC-96, pathogen-derived -- Antigenics
 HSV 863 -- Novartis
 HTLV-I DNA vaccine
 HTLV-I vaccine
 HTLV-II vaccine -- Access
 HU 901 -- Tanox
 Hu23F2G -- ICOS
 HuHMF1
 HumaLYM -- Intracell
 Human krebs statika -- Yamanouchi
 human monoclonal antibodies --
 Abgenix/Biogen, Abgenix/ Corixa,
 Abgenix/immunex, Abgenix/Lexicon,
 Abgenix/ Pfizer, Athersys/Medarex,
 Biogen/MorphoSys, CAT/Searle,
 Centocor/Medarex, Corixa/Kirin Brewery,
 Corixa/Medarex, Eos BioTech./Medarex,
 Eos/Xenerex, Exelixis/Protein Design
 Labs, ImmunoGen/ Raven, Medarex/
 B.Twelve, MorphoSys/ImmunoGen, XTL
 Biopharmaceuticals/Dyax,
 Human monoclonal antibodies --
 Medarex/Northwest Biotherapeutics,
 Medarex/Seattle Genetics
 human netrin-1 -- Exelixis
 human papillomavirus antibodies -- Epicyte
 Human papillomavirus vaccine -- Biotech
 Australia, IDEC, StressGen
 Human papillomavirus vaccine MEDI 501 --
 MedImmune/GlaxoSmithKline
 Human papillomavirus vaccine MEDI
 503/MEDI 504 --
 MedImmune/GlaxoSmithKline
 Human papillomavirus vaccine TA-CIN --
 Cantab Pharmaceuticals
 Human papillomavirus vaccine TA-HPV --
 Cantab Pharmaceuticals
 Human papillomavirus vaccine TH-GW --
 Cantab/GlaxoSmithKline
 human polyclonal antibodies -- Biosite/Eos
 BioTech./ Medarex
 human type II anti factor VIII monoclonal
 antibodies -- ThromboGenics
 humanised anti glycoprotein Ib murine
 monoclonal antibodies -- ThromboGenics
 HumaRAD -- Intracell
 HuMax EGFR -- Genmab
 HuMax-CD4 -- Medarex
 HuMax-IL15 -- Genmab
 HYB 190 -- Hybridon
 HYB 676 -- Hybridon
 I-125 Mab A33 -- Celltech
 Ibritumomab tiuxetan -- IDEC
 IBT-9401 -- Ibx
 IBT-9402 -- Ibx
 IC 14 -- ICOS
 Idarubicin anti-Ly-2.1 --
 IDEC 114 -- IDEC
 IDEC 131 -- IDEC
 IDEC 152 -- IDEC
 IDM 1 -- IDM
 IDPS -- Hollis-Eden Pharmaceuticals

FIG. 28N

45/498

iduronate-2-sulfatase -- Transkaryotic Therapies
 IGF/IBP-2-13 -- Pharis
 IGN-101 -- Igeneon
 IK HIR02 -- Iketon
 IL-11 -- Genetics Institute/AHP
 IL-13-PE38 -- NeoPharm
 IL-17 receptor -- Immunex
 IL-18BP -- Yeda
 IL-1Hy1 -- Hyseq
 IL-1 β -- Celltech
 IL-1 β adjuvant -- Celltech
 IL-2 -- Chiron
 IL-2 + IL-12 -- Hoffman La-Roche
 IL-6/sIL-6R fusion -- Hadasit
 IL-6R derivative -- Tosoh
 IL-7-Dap 389 fusion toxin -- Ligand
 IL-21 -- Novo Nordisk, ZymoGenetics
 IM-862 -- Cytran
 IMC-1C11 -- ImClone
 imiglucerase -- Genzyme
 Immune globulin intravenous (human) -- Hoffman La Roche
 immune privilege factor -- Proneuron
 Immunocal -- Immunotec
 Immunogene therapy -- Briana Bio-Tech
 Immunoliposomal 5-fluorodeoxyuridine-dipalmitate --
 immunosuppressant vaccine -- Aixlie
 immunotoxin -- Antisoma, NIH
 ImmuRAIT-Re-188 -- Immunomedics
 imreg-1 -- Imreg
 infertility -- Johnson & Johnson, E-TRANS
 Infliximab -- Centocor
 Influenza virus vaccine -- Aventis Pasteur, Protein Sciences
 inhibin -- Biotech Australia, Human Therapeutics
 Inhibitory G protein gene therapy
 INKP-2001 -- InKine
 Inolimomab -- Diaclone
 insulin -- AutoImmune, Altea, Biobras, BioSante, Bio-Tech. General, Chong Kun Dang, Emisphere, Flamel, Provalis, Rhein Biotech, TranXenoGen
 insulin (bovine) -- Novartis
 insulin analogue -- Eli Lilly
 Insulin Aspart -- Novo Nordisk
 insulin detemir -- Novo Nordisk
 insulin glargine -- Aventis
 insulin inhaled -- Inhale Therapeutics Systems, Alkermes
 insulin oral -- Inovax
 insulin, AeroDose -- AeroGen
 insulin, AERx -- Aradigm
 insulin, BEODAS -- Elan
 insulin, Biphasix -- Helix
 insulin, buccal -- Generex
 insulin, I2R -- Flemington
 insulin, intranasal -- Bentley
 insulin, oral -- Nobex, Unigene
 insulin, Orasome -- Endorex
 insulin, ProMaxx -- Epic
 insulin, Quadrant -- Elan
 insulin, recombinant -- Aventis
 insulin, Spiros -- Elan
 insulin, Transfersome -- IDEA
 insulin, Zymo, recombinant -- Novo Nordisk
 insulinotropin -- Scios
 Insulysin gene therapy --
 integrin antagonists -- Merck
 interferon (Alpha2) -- SRC VB VECTOR, Viragen, Dong-A, Hoffman La-Roche, Genentech
 interferon -- BioMedicines, Human Genome Sciences
 interferon (Alfa-n3) -- Interferon Sciences Intl.
 interferon (Alpha), Biphasix -- Helix

FIG. 280

46/498

interferon (Alpha)—Amgen, BioNative,
 Novartis, Genzyme Transgenics,
 Hayashibara, Inhale Therapeutics
 Systems, Medusa, Flamel, Dong-A,
 GeneTrol, Nasteck, Shantha,
 Wassermann, LG Chem, Sumitomo,
 Aventis, Behring EGIS, Pepgen, Servier,
 Rhein Biotech,
 interferon (Alpha2A)
 interferon (Alpha2B) — Enzon, Schering-
 Plough, Biogen, IDEA
 interferon (Alpha-N1) — GlaxoSmithKline
 interferon (beta) — Rentschler, GeneTrol,
 Meristem, Rhein Biotech, Toray, Yeda,
 Daiichi, Mochida
 interferon (Beta1A) — Sero, Biogen
 interferon (beta1A), inhale — Biogen
 interferon (β1b)— Chiron
 interferon (tau)— Pepgen
 Interferon alfacon-1 — Amgen
 Interferon alpha-2a vaccine
 Interferon Beta 1b — Schering/Chiron,
 InterMune
 Interferon Gamma — Boehringer Ingelheim,
 Sheffield, Rentschler, Hayashibara
 interferon receptor, Type I — Sero
 interferon (Gamma1B) — Genentech
 Interferon-alpha-2b + ribavirin — Biogen,
 ICN
 Interferon-alpha-2b gene therapy —
 Schering-Plough
 Interferon-con1 gene therapy —
 interleukin-1 antagonists — Dompe
 Interleukin-1 receptor antagonist — Abbott
 Bioresearch, Pharmacia
 Interleukin-1 receptor type I — Immunex
 interleukin-1 receptor Type II — Immunex
 Interleukin-1 trap — Regeneron
 Interleukin-1-alpha — Immunex/Roche
 interleukin-2 — SRC VB VECTOR,
 Ajinomoto, Biomira, Chiron
 IL-2/ diphtheria toxin — Ligand
 Interleukin-3 — Cangene
 Interleukin-4 — Immunology Ventures,
 Sanofi Winthrop, Schering-Plough,
 Immunex/ Sanofi Winthrop, Bayer, Ono
 interleukin-4 + TNF-Alpha — NIH
 interleukin-4 agonist — Bayer
 interleukin-4 fusion toxin — Ligand
 Interleukin-4 receptor — Immunex, Immun
 Interleukin-6 — Ajinomoto, Cangene, Yeda,
 Genetics Institute, Novartis
 interleukin-6 fusion protein
 interleukin-6 fusion toxin — Ligand, Sero
 interleukin-7 — IC Innovations
 interleukin-7 receptor — Immunex
 interleukin-8 antagonists — Kyowa
 Hakko/Millennium/Pfizer
 interleukin-9 antagonists — Genaera
 Interleukin-10 — DNAX, Schering-Plough
 Interleukin-10 gene therapy —
 interleukin-12 — Genetics Institute, Hoffman
 La-Roche
 interleukin-13 — Sanofi
 interleukin-13 antagonists — AMRAD
 Interleukin-13-PE38QQR
 interleukin-15 — Immunex
 interleukin-16 — Research Corp
 Interleukin-18 — GlaxoSmithKline
 Interleukin-18 binding protein — Sero
 Ior-P3 — Center of Molecular Immunology
 IP-10 — NIH
 IPF — Metabolex
 IR-501 — Immune Response
 ISIS 9125 — Isis Pharmaceuticals
 ISURF No. 1554 — Millennium
 ISURF No. 1866 — Iowa State Univer.
 ITF-1697 — Italfarmaco
 IxC 162 — Ixion
 J 695 — Cambridge Antibody Tech.,
 Genetics Inst., Knoll
 Jagged + FGF — Repair

47/498

JKC-362 -- Phoenix Pharmaceuticals
 JTP-2942 -- Japan Tobacco
 Juman monoclonal antibodies --
 Medarex/Raven
 K02 -- Axyx Pharmaceuticals
 Keliximab -- IDEC
 Keyhole limpet haemocyanin
 KGF -- Amgen
 KM 871 -- Kyowa
 KPI 135 -- Scios
 KPI-022 -- Scios
 Kringle 5
 KSB 304
 KSB-201 -- KS Biomedex
 L 696418 -- Merck
 L 703801 -- Merck
 L1 -- Acorda
 L-761191 -- Merck
 lactoferrin -- Meristem, Pharming, Agennix
 lactoferrin cardio -- Pharming
 LAG-3 -- Seroxo
 LAIT -- GEMMA
 LAK cell cytotoxin -- Arizona
 lamellarins -- PharmaMar/University of
 Malaga
 laminin A peptides -- NIH
 lanoteplase -- Genetics Institute
 laronidase -- BioMarin
 Lassa fever vaccine
 LCAT -- NIH
 LDP 01 -- Millennium
 LDP 02 -- Millennium
 Lecithinized superoxide dismutase --
 Seikagaku
 LeIF adjuvant -- Corixa
 leishmaniasis vaccine -- Corixa
 lenercept -- Hoffman La-Roche
 Lenograstim -- Aventis, Chugai
 lepirudin -- Aventis
 leptin -- Amgen, IC Innovations
 Leptin gene therapy -- Chiron Corporation
 leptin, 2nd-generation -- Amgen
 leridistim -- Pharmacia
 leuprolide, ProMaxx -- Epic
 leuprorelin, oral -- Unigene
 LeuTech -- Papatin
 LEX 032 -- SuperGen
 LiDEPT -- Novartis
 Lintuzumab (anti-CD33 MAb) -- Protein
 Design Labs
 lipase -- Altus Biologics
 lipid A vaccine -- EntreMed
 lipid-linked anchor Tech. -- ICRT, ID
 Biomedical
 liposome-CD4 Tech. -- Sheffield
 Listeria monocytogenes vaccine
 LMB 1
 LMB 7
 LMB 9 -- Battelle Memorial Institute, NIH
 LM-CD45 -- Cantab Pharmaceuticals
 lovastatin -- Merck
 LSA-3
 LT- β receptor -- Biogen
 lung cancer vaccine -- Corixa
 lusupultide -- Scios
 L-Vax -- AVAX
 LY 355455 -- Eli Lilly
 LY 366405 -- Eli Lilly
 LY-355101 -- Eli Lilly
 Lyme disease DNA vaccine -- Vical/Aventis
 Pasteur
 Lyme disease vaccine -- Aquila
 Biopharmaceuticals, Aventis, Pasteur,
 Symbicom, GlaxoSmithKline, Hyland
 Immuno, MedImmune
 Lymphocytic choriomeningitis virus vaccine
 lymphoma vaccine -- Biomira, Genitope
 LYP18
 lys plasminogen, recombinant
 Lysosomal storage disease gene therapy --
 Avigen
 lysostaphin -- Nutrition 21

FIG. 28Q

48/498

M 23 -- Gruenenthal
 M1 monoclonal antibodies -- Acorda
 Therapeutics
 MA 16N7C2 -- Corvas Intl.
 malaria vaccine -- GlaxoSmithKline,
 AdProTech, Antigenics, Apovia, Aventis
 Pasteur, Axis Genetics, Behringwerke,
 CDCP, Chiron Vaccines, Genzyme
 Transgenics, Hawaii, MedImmune, NIH,
 NYU, Oxxon, Roche/Saramane, Biotech
 Australia, Rx Tech
 Malaria vaccine CDC/NIIMALVAC-1
 malaria vaccine, multicomponent
 mammaglobin -- Corixa
 mammastatin -- Biotherapeutics
 mannan-binding lectin -- NatlImmu
 mannan-MUC1 -- Psiron
 MAP 30
 Marinovir -- Phytera
 MARstem -- Maret
 MB-015 -- Mochida
 MBP -- ImmuLogic
 MCI-028 -- Mitsubishi-Tokyo
 MCIF -- Human Genome Sciences
 MDC -- Advanced BioScience -- Akzo
 Nobel, ICOS
 MDX 11 -- Medarex
 MDX 210 -- Medarex
 MDX 22 -- Medarex
 MDX 22
 MDX 240 -- Medarex
 MDX 33
 MDX 44 -- Medarex
 MDX 447 -- Medarex
 MDX H210 -- Medarex
 MDX RA -- Houston BioTech., Medarex
 ME-104 -- Pharmexa
 Measles vaccine
 Mecasermin -- Cephalon/Chiron, Chiron
 MEDI 488 -- MedImmune
 MEDI 500
 MEDI 507 -- BioTransplant
 melanin concentrating hormone --
 Neurocrine Biosciences
 melanocortins -- OMRF
 Melanoma monoclonal antibodies -- Viragen
 melanoma vaccine -- GlaxoSmithKline,
 Akzo Nobel, Avant, Aventis Pasteur,
 Bavarian Nordic, Biovector, CancerVax,
 Genzyme Molecular Oncology, Humbolt,
 ImClone Systems, Memorial, NYU, Oxxon
 Melanoma vaccine Magevac -- Therion
 memory enhancers -- Scios
 meningococcal B vaccine -- Chiron
 meningococcal vaccine -- CAMR
 Meningococcal vaccine group B conjugate -
 - North American Vaccine
 Meningococcal vaccine group B
 recombinant -- BioChem Vaccines,
 Microscience
 Meningococcal vaccine group Y conjugate -
 - North American Vaccine
 Meningococcal vaccine groups A B and C
 conjugate -- North American Vaccine
 Mepolizumab -- GlaxoSmithKline
 Metastatin -- EntreMed, Takeda
 Met-CkB7 -- Human Genome Sciences
 met-enkephalin -- TNI
 METH-1 -- Human Genome Sciences
 methioninase -- AntiCancer
 Methionine lyase gene therapy --
 AntiCancer
 Met-RANTES -- Genexa Biomedical,
 Seroxo
 Metreleptin
 Microtubule inhibitor MAb
 Immunogen/Abgenix
 MGDF -- Kirin
 MGv -- Progenics
 micrin -- Endocrine
 microplasmin -- ThromboGenics
 MIF -- Genetics Institute

FIG. 28R

49/498

migration inhibitory factor -- NIH	MAb 45-2D9- -- haematoporphyrin conjugate
Mim CD4.1 -- Xycte Therapies	MAb 4B4
mirostipen -- Human Genome Sciences	MAb 4E3-CPA conjugate -- BCM Oncologia
Mitumomab (BEC-2) -- ImClone Systems, Merck KGaA	MAb 4E3-daunorubicin conjugate
MK 852 -- Merck	MAb 50-6
MLN 1202 (Anti-CCR2 monoclonal antibody) -- Millenium Pharmaceuticals	MAb 50-61A -- Institut Pasteur
Mobenakin -- NIS	MAb 5A8 -- Biogen
molgramostim -- Genetics Institute, Novartis	MAb 791T/36-methotrexate conjugate
monoclonal antibodies -- Abgenix/Celltech, Immusol/ Medarex, Viragen/ Roslin Institute, Cambridge Antibody Tech./Elan	MAb 7c11.e8
MAb 108 --	MAb 7E11 C5-selenocystamine conjugate
MAb 10D5 --	MAb 93KA9 -- Novartis
MAb 14.18-interleukin-2 immunocytokine -- Lexigen	MAb A5B7-cisplatin conjugate -- Biodynamics Research, Pharmacia
MAb 14G2a --	MAb A5B7-I-131
MAb 15A10 --	MAb A7
MAb 170 -- Biomira	MAb A717 -- Exocell
MAb 177Lu CC49 --	MAb A7-zinostatin conjugate
MAb 17F9	MAb ABX-RB2 -- Abgenix
MAb 1D7	MAb ACA 11
MAb 1F7 -- Immune Network	MAb AFP-I-131 -- Immunomedics
MAb 1H10-doxorubicin conjugate	MAb AP1
MAb 26-2F	MAb AZ1
MAb 2A11	MAb B3-LysPE40 conjugate
MAb 2E1 -- RW Johnson	MAb B4 -- United Biomedical
MAb 2F5	MAb B43 Genistein-conjugate
MAb 31.1 -- International BioImmune Systems	MAb B43.13-Tc-99m -- Biomira
MAb 32 -- Cambridge Antibody Tech., Peptech	MAb B43-PAP conjugate
MAb 323A3 -- Centocor	MAb B4G7-gelonin conjugate
MAb 3C5	MAb BCM 43-daunorubicin conjugate -- BCM Oncologia
MAb 3F12	MAb BIS-1
MAb 3F8	MAb BMS 181170 -- Bristol-Myers Squibb
MAb 42/6	MAb BR55-2
MAb 425 -- Merck KGaA	MAb BW494
MAb 447-52D -- Merck Sharp & Dohme	MAb C 242-DM1 conjugate -- ImmunoGen
	MAb C242-PE conjugate
	MAb c30-6
	MAb CA208-cytorhodin-S conjugate -- Hoechst Japan
	MAb CC49 -- Enzo

FIG. 28S

50/498

MAb ch14.18 --	MAb LL2-I-131 -- Immunomedics
MAb CH14.18-GM-CSF fusion protein -- Lexigen	MAb LL2-Y-90
MAb chCE7	MAb LS2D617 -- Hybritech
MAb CI-137 -- AMRAD	MAb LYM-1-gelonin conjugate
MAb cisplatin conjugate	MAb LYM-1-I-131
MAb CLB-CD19	MAb LYM-1-Y-90
MAb CLB-CD19v	MAb LYM-2 -- Peregrine
MAb CLL-1 -- Peregrine	MAb M195
MAb CLL-1-GM-CSF conjugate	MAb M195-bismuth 213 conjugate -- Protein Design Labs
MAb CLL-1-IL-2 conjugate -- Peregrine	MAb M195-gelonin conjugate
MAb CLN IgG -- doxorubicin conjugates	MAB M195-I-131
MAB conjugates -- Tanox	MAB M195-Y-90
MAB D612	MAB MA 33H1 -- Sanofi
MAB Dal B02	MAB MAD11
MAB DC101 -- ImClone	MAB MGB2
MAB EA 1 --	MAB MINT5
MAB EC708 -- Biovation	MAB MK2-23
MAB EP-5C7 -- Protein Design Labs	MAB MOC31 ETA(252-613) conjugate
MAB ERIC-1 -- ICRT	MAB MOC-31-In-111
MAB F105 gene therapy	MAB MOC-31-PE conjugate
MAB FC 2.15	MAB MR6 --
MAB G250 -- Centocor	MAB MRK-16 -- Aventis Pasteur
MAB GA6	MAB MS11G6
MAB GA733	MAB MX-DTPA BrE-3
MAB Gliomab-H -- Viventia Biotech	MAB MY9
MAB HB2-saporin conjugate	MAB Nd2 -- Tosoh
MAB HD 37 --	MAB NG-1 -- Hygeia
MAB HD37-ricin chain-A conjugate	MAB NM01 -- Nissin Food
MAB HNK20 -- Acambis	MAB OC 125
MAB huN901-DM1 conjugate -- ImmunoGen	MAB OC 125-CMA conjugate
MAB I-131 CC49 -- Corixa	MAB OKI-1 -- Ortho-McNeil
MAB ICO25	MAB OX52 -- Bioproducts for Science
MAB ICR12-CPG2 conjugate	MAB PMA5
MAB ICR-62	MAB PR1
MAB IRac-ricin A conjugate	MAB prost 30
MAB K1	MAB R-24
MAB KS1-4-methotrexate conjugate	MAB R-24 α Human GD3 -- Celltech
MAB L6 -- Bristol-Myers Squibb, Oncogen	MAB RFB4-ricin chain A conjugate
MAB LICO 16-88	MAB RFT5-ricin chain A conjugate
	MAB SC 1

FIG. 28T

51/498

MAb SM-3 -- ICRT
 MAb SMART 1D10 -- Protein Design Labs
 MAb SMART ABL 364 -- Novartis
 MAb SN6f
 MAb SN6f-deglycosylated ricin A chain conjugate --
 MAb SN6j
 MAb SN7-ricin chain A conjugate
 MAb T101-Y-90 conjugate -- Hybritech
 MAb T-88 -- Chiron
 MAb TB94 -- Cancer Immunobiology
 MAb TEC 11
 MAb TES-23 -- Chugai
 MAb TM31 -- Avant
 MAb TNT-1 -- Cambridge Antibody Tech., Peregrine
 MAb TNT-3
 MAb TNT-3 -- IL2 fusion protein --
 MAb TP3-At-211
 MAb TP3-PAP conjugate --
 MAb UJ13A -- ICRT
 MAb UN3
 MAb ZME-018-gelonin conjugate
 MAb-BC2 -- GlaxoSmithKline
 MAb-DM1 conjugate -- ImmunoGen
 MAb-ricin-chain-A conjugate -- XOMA
 MAb-temoporfin conjugates
 Monopharm C -- Viventia Biotech
 montepelase -- Eisai
 montirelin hydrate -- Gruenenthal
 morotocog alfa -- Genetics Institute
 Morotocog-alfa -- Pharmacia
 MP 4
 MP-121 -- Biopharm
 MP-52 -- Biopharm
 MRA -- Chugai
 MS 28168 -- Mitsui Chemicals, Nihon Schering
 MSH fusion toxin -- Ligand
 MSI-99 -- Genæra
 MT 201 -- Micromet
 Muc-1 vaccine -- Corixa
 mucosal tolerance -- Aberdeen
 mullerian inhibiting subst
 muplestim -- Genetics Institute, Novartis,
 DSM Anti-Infectives
 murine MAb -- KS Biomedix
 Mutant somatropin -- JCR Pharmaceutical
 MV 833 -- Toagosei
 Mycoplasma pulmonis vaccine
 Mycoprex -- XOMA
 myeloperoxidase -- Henogen
 myostatin -- Genetics Institute
 Nacolomab tafenatox -- Pharmacia
 Nagrecor -- Scios
 nagrestipen -- British Biotech
 NAP-5 -- Corvas Intl.
 NAPc2 -- Corvas Intl.
 nartograstim -- Kyowa
 Natalizumab -- Protein Design Labs
 Nateplase -- NIH, Nihon Schering
 nateplase -- Schering AG
 NBI-3001 -- Neurocrine Biosci.
 NBI-5788 -- Neurocrine Biosci.
 NBI-6024 -- Neurocrine Biosci.
 Nef inhibitors -- BRI
 Neisseria gonorrhoea vaccine -- Antex Biologics
 Neomycin B-arginine conjugate
 Nerelimomab -- Chiron
 Nerve growth factor -- Amgen -- Chiron, Genentech
 Nerve growth factor gene therapy
 nesiritide citrate -- Scios
 neuregulin-2 -- CeNeS
 neurocan -- NYU
 neuronal delivery system -- CAMR
 Neurophil inhibitory Factor -- Corvas
 Neuroprotective vaccine -- University of Auckland
 neurotrophic chimaeras -- Regeneron
 neurotrophic factor -- NsGene, CereMedix

FIG. 28U

52/498

NeuroVax -- Immune Response
 neurturnin -- Genentech
 neutral endopeptidase -- Genentech
 NGF enhancers -- NeuroSearch
 NHL vaccine -- Large Scale Biology
 NIP45 -- Boston Life Sciences
 NKI-B20
 NM 01 -- Nissin Food
 NMI-139 -- NitroMed
 NMMP -- Genetics Institute
 NN-2211 -- Novo Nordisk
 Noggin -- Regeneron
 Nonacog alfa
 Norelin -- Biostar
 Norwalk virus vaccine
 NRLU 10 -- NeoRx
 NRLU 10 PE -- NeoRx
 NT-3 -- Regeneron
 NT-4/5 -- Genentech
 NU 3056
 NU 3076
 NX 1838 -- Gilead Sciences
 NY ESO-1/CAG-3 antigen -- NIH
 NYVAC-7 -- Aventis Pasteur
 NZ-1002 -- Novazyme
 obesity therapy -- Nobex
 OC 10426 -- Ontogen
 OC 144093 -- Ontogen
 OCIF -- Sankyo
 Oct-43 -- Otsuka
 Odulimomab -- Immunotech
 OK PSA - liposomal
 OKT3-gamma-1-ala-ala
 OM 991
 OM 992
 Omalizumab -- Genentech
 oncoimmunin-L -- NIH
 Oncolysin B -- ImmunoGen
 Oncolysin CD6 -- ImmunoGen
 Oncolysin M -- ImmunoGen
 Oncolysin S -- ImmunoGen
 Oncophage -- Antigenics
 Oncostatin M -- Bristol-Myers Squibb
 OncoVax-CL -- Jenner Biotherapies
 OncoVax-P -- Jenner Biotherapies
 onercept -- Yeda
 onychomycosis vaccine -- Boehringer
 Ingelheim
 opebecan -- XOMA
 opioids -- Arizona
 Oprelvekin -- Genetics Institute
 Oregovomab -- AltaRex
 Org-33408 b-- Akzo Nobel
 Orlip DP -- EpiCept
 oryzacystatin
 OSA peptides -- GenSci Regeneration
 osteoblast-cadherin GF -- Pharis
 Osteocalcin-thymidine kinase gene therapy
 osteogenic protein -- Curis
 osteopontin -- OraPharma
 osteoporosis peptides -- Integra, Telios
 osteoprotegerin -- Amgen, SnowBrand
 otitis media vaccines -- Antex Biologics
 ovarian cancer -- University of Alabama
 OX40-IgG fusion protein -- Cantab, Xenova
 P 246 -- Diatide
 P 30 -- Alfacell
 p1025 -- Active Biotech
 P-113^A -- Demegen
 P-16 peptide -- Transition Therapeutics
 p43 -- Ramot
 P-50 peptide -- Transition Therapeutics
 p53 + RAS vaccine -- NIH, NCI
 PACAP(1-27) analogue
 paediatric vaccines -- Chiron
 Pafase -- ICOS
 PAGE-4 plasmid DNA -- IDEC
 PAI-2 -- Biotech Australia, Human
 Therapeutics
 Palifermin (keratinocyte growth factor) --
 Amgen
 Palivizumab -- MedImmune

FIG. 28V

53/498

PAM 4 -- Merck
 pamiteplase -- Yamanouchi
 pancreatin, Minitabs -- Eurand
 Pangen -- Fournier
 Pantarin -- Selective Genetics
 Parainfluenza virus vaccine -- Pharmacia,
 Pierre Fabre
 paraoxanase -- Esperion
 parathyroid hormone -- Abiogen, Korea
 Green Cross
 Parathyroid hormone (1-34) --
 Chugai/Suntory
 Parkinson's disease gene therapy -- Cell
 Genesys/ Ceregene
 Parvovirus vaccine -- MedImmune
 PCP-Scan -- Immunomedics
 PDGF -- Chiron
 PDGF cocktail -- Theratechnologies
 peanut allergy therapy -- Dynavax
 PEG anti-ICAM MAb -- Boehringer
 Ingelheim
 PEG asparaginase -- Enzon
 PEG glucocerebrosidase
 PEG hirudin -- Knoll
 PEG interferon-alpha-2a -- Roche
 PEG interferon-alpha-2b + ribavirin --
 Biogen, Enzon, ICN Pharmaceuticals,
 Schering-Plough
 PEG MAb A5B7 --
 Pegacaristim -- Amgen -- Kirin Brewery --
 ZymoGenetics
 Pegaldesleukin -- Research Corp
 pegaspargase -- Enzon
 pegfilgrastim -- Amgen
 PEG-interferon Alpha -- Viragen
 PEG-interferon Alpha 2A -- Hoffman La-
 Roche
 PEG-interferon Alpha 2B -- Schering-
 Plough
 PEG-r-hirudin -- Abbott
 PEG-rHuMGDF -- Amgen
 PEG-uricase -- Mountain View
 Pegvisomant -- Genentech
 PEGylated proteins, PolyMASC -- Valentis
 PEGylated recombinant native human leptin
 -- Roche
 Pentumomab
 Penetratin -- Cyclacel
 Pepscan -- Antisoma
 peptide G -- Peptech, ICRT
 peptide vaccine -- NIH, NCJ
 Pexelizumab
 pexiganan acetate -- Genaera
 Pharmaprojects No. 3179 -- NYU
 Pharmaprojects No. 3390 -- Ernest Orlando
 Pharmaprojects No. 3417 -- Sumitomo
 Pharmaprojects No. 3777 -- Acambis
 Pharmaprojects No. 4209 -- XOMA
 Pharmaprojects No. 4349 -- Baxter Intl.
 Pharmaprojects No. 4651
 Pharmaprojects No. 4915 -- Avanir
 Pharmaprojects No. 5156 -- Rhizogenics
 Pharmaprojects No. 5200 -- Pfizer
 Pharmaprojects No. 5215 -- Origene
 Pharmaprojects No. 5216 -- Origene
 Pharmaprojects No. 5218 -- Origene
 Pharmaprojects No. 5267 -- ML
 Laboratories
 Pharmaprojects No. 5373 -- MorphoSys
 Pharmaprojects No. 5493 -- Metabolex
 Pharmaprojects No. 5707 -- Genentech
 Pharmaprojects No. 5728 -- Autogen
 Pharmaprojects No. 5733 -- BioMarin
 Pharmaprojects No. 5757 -- NIH
 Pharmaprojects No. 5765 -- Gryphon
 Pharmaprojects No. 5830 -- AntiCancer
 Pharmaprojects No. 5839 -- Dyax
 Pharmaprojects No. 5849 -- Johnson &
 Johnson
 Pharmaprojects No. 5860 -- Mitsubishi-
 Tokyo

FIG. 28W

54/498

- Pharmaprojects No. 5869 -- Oxford GlycoSciences
- Pharmaprojects No. 5883 -- Asahi Brewery
- Pharmaprojects No. 5947 -- StressGen
- Pharmaprojects No. 5961 -- Theratechnologies
- Pharmaprojects No. 5962 -- NIH
- Pharmaprojects No. 5966 -- NIH
- Pharmaprojects No. 5994 -- Pharming
- Pharmaprojects No. 5995 -- Pharming
- Pharmaprojects No. 6023 -- IMMUCON
- Pharmaprojects No. 6063 -- Cytoclonal
- Pharmaprojects No. 6073 -- SIDDCO
- Pharmaprojects No. 6115 -- Genzyme
- Pharmaprojects No. 6227 -- NIH
- Pharmaprojects No. 6230 -- NIH
- Pharmaprojects No. 6236 -- NIH
- Pharmaprojects No. 6243 -- NIH
- Pharmaprojects No. 6244 -- NIH
- Pharmaprojects No. 6281 -- Senetek
- Pharmaprojects No. 6365 -- NIH
- Pharmaprojects No. 6368 -- NIH
- Pharmaprojects No. 6373 -- NIH
- Pharmaprojects No. 6408 -- Pan Pacific
- Pharmaprojects No. 6410 -- Athersys
- Pharmaprojects No. 6421 -- Oxford GlycoSciences
- Pharmaprojects No. 6522 -- Maxygen
- Pharmaprojects No. 6523 -- Pharis
- Pharmaprojects No. 6538 -- Maxygen
- Pharmaprojects No. 6554 -- APALEXO
- Pharmaprojects No. 6560 -- Ardana
- Pharmaprojects No. 6562 -- Bayer
- Pharmaprojects No. 6569 -- Eos
- Phenoxazine
- Phenylase -- Ibbex
- Pigment epithelium derived factor -- plasminogen activator inhibitor-1, recombinant -- DuPont Pharmaceuticals
- Plasminogen activators -- Abbott Laboratories, American Home Products, Boehringer Mannheim, Chiron Corporation, DuPont Pharmaceuticals, Eli Lilly, Shionogi, Genentech, Genetics Institute, GlaxoSmithKline, Hemispherx Biopharma, Merck & Co, Novartis, Pharmacia Corporation, Wakamoto, Yeda
- plasminogen-related peptides -- Bio-Tech. General/MGH
- platelet factor 4 -- RepliGen
- Platelet-derived growth factor -- Amgen -- ZymoGenetics
- plusonemin -- Hayashibara
- PMD-2850 -- Protherics
- Pneumococcal vaccine -- Antex Biologics, Aventis Pasteur
- Pneumococcal vaccine intranasal -- BioChem Vaccines/Biovector
- PR1A3
- PR-39
- pralmorelin -- Kaken
- Pretarget-Lymphoma -- NeoRx
- Priliximab -- Centocor
- PRO 140 -- Progenics
- PRO 2000 -- Procept
- PRO 367 -- Progenics
- PRO 542 -- Progenics
- pro-Apo A-I -- Esperion
- prolactin -- Genzyme
- Prosaptide TX14(A) -- Bio-Tech. General
- prostate cancer antibodies -- Immunex, UroCor
- prostate cancer antibody therapy -- Genentech/UroGenesys, Genotherapeutics
- prostate cancer immunotherapeutics -- The PSMA Development Company
- prostate cancer vaccine -- Aventis Pasteur, Zonagen, Corixa, Dendreon, Jenner
- Biotherapies, Therion Biologics

FIG. 28X

55/498

prostate-specific antigen -- Entremed
 protein A -- RepliGen
 protein adhesives -- Enzon
 protein C -- Baxter Intl., PPL Therapeutics,
 ZymoGenetics
 protein C activator -- Gilead Sciences
 protein kinase R antagonists -- NIH
 protirelin -- Takeda
 protocadherin 2 -- Caprion
 Pro-urokinase -- Abbott, Bristol-Myers
 Squibb, Dainippon, Tosoh -- Welfide
 P-selectin glycoprotein ligand-1 -- Genetics
 Institute
 pseudomonal infections -- InterMune
 Pseudomonas vaccine -- CytoVax
 PSGL-Ig -- American Home Products
 PSP-94 -- Procyon
 PTH 1-34 -- Nobex
 Quilimmune-M -- Antigenics
 R 744 -- Roche
 R 101933
 R 125224 -- Sankyo
 RA therapy -- Cardion
 Rabies vaccine recombinant -- Aventis
 Pasteur, BioChem Vaccines, Kaketsuken
 Pharmaceuticals
 RadioTheraCIM -- YM BioSciences
 Ramot project No. 1315 -- Ramot
 Ramot project No. K-734A -- Ramot
 Ramot project No. K-734B -- Ramot
 Ranibizumab (Anti-VEGF fragment) --
 Genentech
 RANK -- Immunex
 ranpirinase -- Alfacell
 ranpirinase-anti-CD22 MAb -- Alfacell
 RANTES inhibitor -- Milan
 RAPID drug delivery systems -- ARIAD
 rasburicase -- Sanofi
 rBPI-21, topical -- XOMA
 RC 529 -- Corixa
 rCFTR -- Genzyme Transgenics

RD 62198
 rDnase -- Genentech
 RDP-58 -- SangStat
 RecepTox-Fce -- Keryx
 RecepTox-GnRH -- Keryx, MTR
 Technologies
 RecepTox-MBP -- Keryx, MTR
 Technologies
 recFSH -- Akzo Nobel, Organon
 REGA 3G12
 Regavirumab -- Teijin
 relaxin -- Connetics Corp
 Renal cancer vaccine -- MacroPharm
 repifermin -- Human Genome Sciences
 Respiratory syncytial virus PFP-2 vaccine --
 Wyeth-Lederle
 Respiratory syncytial virus vaccine --
 GlaxoSmithKline, Pharmacia, Pierre Fabre
 Respiratory syncytial virus vaccine
 inactivated
 Respiratory syncytial virus-parainfluenza
 virus vaccine -- Aventis Pasteur,
 Pharmacia
 Reteplase -- Boehringer Mannheim,
 Hoffman La-Roche
 Retropep -- Retroscreen
 RFB4 (dsFv) PE38
 RFI 641 -- American Home Products
 RFTS -- UAB Research Foundation
 RG 12986 -- Aventis Pasteur
 RG 83852 -- Aventis Pasteur
 RG-1059 -- RepliGen
 rGCR -- NIH
 rGLP-1 -- Restoragen
 rGRF -- Restoragen
 rh Insulin -- Eli Lilly
 RHAMM targeting peptides -- Cangene
 rHb1.1 -- Baxter Intl.
 rhCC10 -- Claragen
 rhCG -- SeroNo
 Rheumatoid arthritis gene therapy

FIG. 28Y

56/498

Rheumatoid arthritis vaccine -- Veterans

Affairs Medical Center

rhLH -- Serono

Ribozyme gene therapy -- Genset

Rickettsial vaccine recombinant

RIGScan CR -- Neoprobe

RIP-3 -- Rigel

Rituximab -- Genentech

RK-0202 -- RxKinetix

RLT peptide -- Esperion

rM/NEI -- IVAX

rmCRP -- Immtech

RN-1001 -- Renovo

RN-3 -- Renovo

RNase conjugate -- Immunomedics

RO 631908 -- Roche

Rotavirus vaccine -- Merck

RP 431 -- DuPont Pharmaceuticals

RP-128 -- Resolution

RPE65 gene therapy --

RPR 110173 -- Aventis Pasteur

RPR 115135 -- Aventis Pasteur

RPR 116258A -- Aventis Pasteur

rPSGL-Ig -- American Home Products

r-SPC surfactant -- Byk Gulden

RSV antibody -- Medimmune

Ruplizumab -- Biogen

rV-HER-2/neu -- Therion Biologics

SA 1042 -- Sankyo

sacrosidase -- Orphan Medical

Sant 7

Sargramostim -- Immunex

saruplase -- Gruenthal

Satumomab -- Cytogen

SB 1 -- COR Therapeutics

SB 207448 -- GlaxoSmithKline

SB 208651 -- GlaxoSmithKline

SB 240683 -- GlaxoSmithKline

SB 249415 -- GlaxoSmithKline

SB 249417 -- GlaxoSmithKline

SB 6 -- COR Therapeutics

SB RA 31012 --

SC 56929 -- Pharmacia

SCA binding proteins -- Curis, Enzon

scFv(14E1)-ETA Berlex Laboratories,

Schering AG

ScFv(FRP5)-ETA --

ScFv6C6-PE40 --

SCH 55700 -- Celltech

Schistosomiasis vaccine -- Glaxo

Wellcome/Medeva, Brazil

SCPF -- Advanced Tissue Sciences

scuPA-suPAR complex -- Hadasit

SD-9427 -- Pharmacia

SDF-1 -- Ono

SDZ 215918 -- Novartis

SDZ 280125 -- Novartis

SDZ 89104 -- Novartis

SDZ ABL 364 -- Novartis

SDZ MMA 383 -- Novartis

Secretin -- Ferring, Repligen

serine protease inhbs -- Pharis

sermorelin acetate -- Sero

SERP-1 -- Viron

sertenef -- Dainippon

serum albumin, Recombinant human --

Aventis Behring

serum-derived factor -- Hadasit

Sevirumab -- Novartis

SGN 14 -- Seattle Genetics

SGN 15 -- Seattle Genetics

SGN 17/19 -- Seattle Genetics

SGN 30 -- Seattle Genetics

SGN-10 -- Seattle Genetics

SGN-11 -- Seattle Genetics

SH 306 -- DuPont Pharmaceuticals

Shanvac-B -- Shantha

Shigella flexneri vaccine -- Avant, Acambis,

Novavax

Shigella sonnei vaccine --

sICAM-1 -- Boehringer Ingelheim

Silteplase -- Genzyme

FIG. 28Z

57/498

SIV vaccine -- Endocon, Institut Pasteur
 SK 896 -- Sanwa Kagaku Kenkyusho
 SK-827 -- Sanwa Kagaku Kenkyusho
 Skeletex -- CellFactors
 SKF 106160 -- GlaxoSmithKline
 S-nitroso-AR545C --
 SNTP -- Active Biotech
 somatomedin-1 -- GroPep, Mitsubishi-
 Tokyo, NIH
 somatomedin-1 carrier protein -- Insmed
 somatostatin -- Ferring
 Somatotropin/
 Human Growth Hormone -- Bio-Tech.
 General, Eli Lilly
 somatropin -- Bio-Tech. General, Alkermes,
 ProLease, Aventis Behring, Biovector,
 Cangene, Dong-A, Eli Lilly, Emisphere,
 Enact, Genentech, Genzyme Transgenics,
 Grandis/InfiMed, CSL, InfiMed, MacroMed,
 Novartis, Novo Nordisk, Pharmacia
 Serono, TranXenoGen
 somatropin derivative -- Schering AG
 somatropin, AIR -- Eli Lilly
 Somatropin, inhaled -- Eli Lilly/Alkermes
 somatropin, Kabi -- Pharmacia
 somatropin, Orasome -- Novo Nordisk
 Sonermin -- Daiippon Pharmaceutical
 SP(V5.2)C -- Supertek
 SPf66
 sphingomyelinase -- Genzyme
 SR 29001 -- Sanofi
 SR 41476 -- Sanofi
 SR-29001 -- Sanofi
 SS1(dsFV)-PE38 -- NeoPharm
 β 2 microglobulin -- Avidex
 β 2-microglobulin fusion proteins -- NIH
 β -amyloid peptides -- CeNeS
 β -defensin -- Pharis
 Staphylococcus aureus infections --
 Inhibibex/ZLB
 Staphylococcus aureus vaccine conjugate --
 Nabi
 Staphylococcus therapy -- Tripep
 Staphylokinase -- Biovation, Prothera,
 Thrombogenetics
 Streptococcal A vaccine -- M6
 Pharmaceuticals, North American Vaccine
 Streptococcal B vaccine -- Microscience
 Streptococcal B vaccine recombinant --
 Biochem Vaccines
 Streptococcus pyogenes vaccine
 STRL-33 -- NIH
 Subalin -- SRC VB VECTOR
 SUIIS -- United Biomedical
 SUIIS-LHRH -- United Biomedical
 SUN-E3001 -- Suntory
 super high affinity monoclonal antibodies --
 YM BioSciences
 Superoxide dismutase -- Chiron, Enzon,
 Ube Industries, Bio-Tech, Yeda
 superoxide dismutase-2 -- OXIS
 suppressin -- UAB Research Foundation
 SY-161-P5 -- ThromboGenics
 SY-162 -- ThromboGenics
 Systemic lupus erythematosus vaccine --
 MedClone/VivoRx
 T cell receptor peptides -- Xoma
 T cell receptor peptide vaccine
 T4N5 liposomes -- AGI Dermatics
 TACI, soluble -- ZymoGenetics
 targeted apoptosis -- Antisoma
 tasonermin -- Boehringer Ingelheim
 TASP
 TASP-V
 Tat peptide analogues -- NIH
 TBP I -- Yeda
 TBP II
 TBV25H -- NIH
 Tc 99m ior cea1 -- Center of Molecular
 Immunology
 Tc 99m P 748 -- Diatide

FIG. 28AA

58/498

Tc 99m votumab -- Intracell
 Tc-99m rh-Annexin V -- Theseus Imaging
 teceleukin -- Biogen
 tenecteplase -- Genentech
 Teriparatide -- Armour Pharmaceuticals,
 Asahi Kasei, Eli Lilly
 terlipressin -- Ferring
 testisin -- AMRAD
 Tetra fibrin -- Roche
 TFPI -- EntrelMed
 tgD-IL-2 -- Takeda
 TGF-Alpha -- ZymoGenetics
 TGF- β -- Kolon
 TGF- β 2 -- Insmad
 TGF- β 3 -- OSI
 Thalassemia gene therapy -- Crucell
 TheraCIM-h-R3 -- Center of Molecular
 Immunology, YM BioSciences
 Theradigm-HBV -- Epimmune
 Theradigm-HPV -- Epimmune
 Theradigm-malaria -- Epimmune
 Theradigm-melanoma -- Epimmune
 TheraFab -- Antisoma
 ThGRF 1-29 -- Theratechnologies
 ThGRF 1-44 -- Theratechnologies
 Thrombin receptor activating peptide --
 Abbott
 thrombomodulin -- Iowa, Novocastra
 Thrombopoietin -- Dragon Pharmaceuticals,
 Genentech
 thrombopoietin, Pliva -- Recepton
 Thrombospondin 2 --
 thrombostatin -- Thromgen
 thymalfasin -- SciClone
 thymocartin -- Gedeon Richter
 thymosin Alpha1 -- NIH
 thyroid stimulating hormone -- Genzyme
 tICAM-1 -- Bayer
 Tick anticoagulant peptide -- Merck
 TIF -- Xoma
 Tifacogin -- Chiron, NIS, Pharmacia
 Tissue factor -- Genentech
 Tissue factor pathway inhibitor
 TJN-135 -- Tsumura
 TM 27 -- Avant
 TM 29 -- Avant
 TMC-151 -- Tanabe Seiyaku
 TNF tumour necrosis factor -- Asahi Kasei
 TNF Alpha -- CytImmune
 TNF antibody -- Johnson & Johnson
 TNF binding protein -- Amgen
 TNF degradation product -- Oncotech
 TNF receptor -- Immunex
 TNF receptor 1, soluble -- Amgen
 TNF Tumour necrosis factor-alpha -- Asahi
 Kasei, Genentech, Mochida
 TNF-Alpha inhibitor -- Tripep
 TNFR:Fc gene therapy -- Targeted Genetics
 TNF-SAM2
 Tolerimab -- Innogenetics
 Toxoplasma gondii vaccine --
 GlaxoSmithKline
 TP 9201 -- Telios
 TP10 -- Avant
 TP20 -- Avant
 tPA -- Centocor
 trafermin -- Scios
 TRAIL/Apo2L -- Immunex
 TRAIL-R1 MAb -- Cambridge Antibody
 Technologies
 transferrin-binding proteins -- CAMR
 Transforming growth factor-beta-1 --
 Genentech
 transport protein -- Genesis
 Trastuzumab -- Genentech
 TRH -- Ferring
 Triabin -- Schering AG
 Triconal
 Triflavin
 troponin I -- Boston Life Sciences
 TRP-2^A -- NIH
 trypsin inhibitor -- Mochida

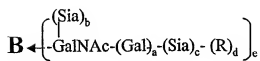
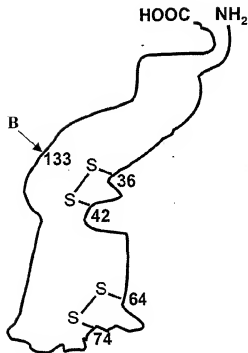
FIG. 28BB

59/498

<p>TSP-1 gene therapy – TT-232 TTS-CD2 -- Active Biotech Tuberculosis vaccine -- Aventis Pasteur, Genesis Tumor Targeted Superantigens -- Active Biotech -- Pharmacia tumour vaccines -- PhotoCure tumour-activated prodrug antibody conjugates -- Millennium/ImmunoGen tumstatin -- ILEX Tuvirumab -- Novartis TV-4710 -- Teva TWEAK receptor -- Immunex TXU-PAP TY-10721 -- TOA Eiyo Type I diabetes vaccine -- Research Corp Typhoid vaccine CVD 908 U 143677 -- Pharmacia U 81749 -- Pharmacia UA 1248 -- Arizona UGIF -- Sheffield UIC 2 UK 101 UK-279276 -- Corvas Intl. urodilatin -- Pharis urofollitrophin -- Serono Urokinase -- Abbott uteroferin-- Pepgen V 20 -- GLYCODesign V2 vasopressin receptor gene therapy vaccines -- Active Biotech Varicella zoster glycoprotein vaccine -- Research Corporation Technologies Varicella zoster virus vaccine live -- Cantab Pharmaceuticals Vascular endothelial growth factor -- Genentech, University of California</p>	<p>Vascular endothelial growth factors -- R&D Systems vascular targeting agents -- Peregrine vasopermeation enhancement agents -- Peregrine vasostatin -- NIH VCL -- Bio-Tech. General VEGF -- Genentech, Scios VEGF inhibitor -- Chugai VEGF-2 -- Human Genome Sciences VEGF-Trap -- Regeneron viscumin, recombinant -- Madaus Vitaxin Vitraxe -- ISTA Pharmaceuticals West Nile virus vaccine -- Bavarian Nordic WP 652 WT1 vaccine -- Corixa WX-293 -- Wilex BioTech. WX-360 -- Wilex BioTech. WX-UK1 -- Wilex BioTech. XMP-500 -- XOMA XomaZyme-791 -- XOMA XTL 001 -- XTL Biopharmaceuticals XTL 002 -- XTL Biopharmaceuticals yeast delivery system -- GlobelImmune Yersinia pestis vaccine YIGSR-Stealth -- Johnson & Johnson Yissum Project No. D-0460 -- Yissum YM 207 -- Yamanouchi YM 337 -- Protein Design Labs Yttrium-90 labelled biotin Yttrium-90-labeled anti-CEA MAb T84.66 -- ZD 0490 -- AstraZeneca ziconotide -- Elan ZK 157138 -- Berlex Laboratories Zolimomab arixox Zorcell -- Immune Response ZRXL peptides -- Novartis</p>
--	---

FIG. 28CC

60/498



a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, sialyl or oligosialyl

FIG. 29A

61/498

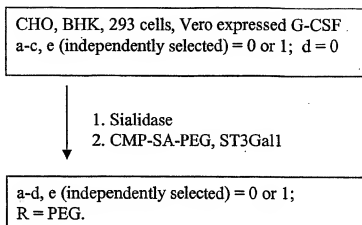


FIG. 29B

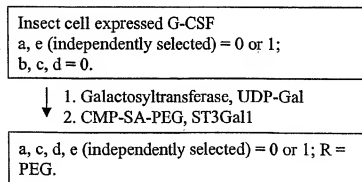


FIG. 29C

62/498

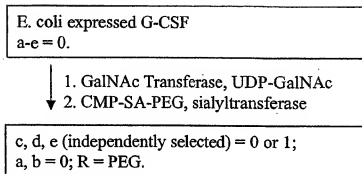


FIG. 29D

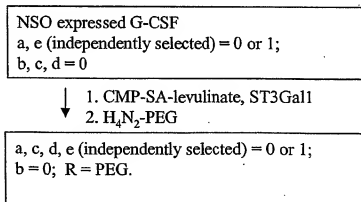


FIG. 29E

63/498

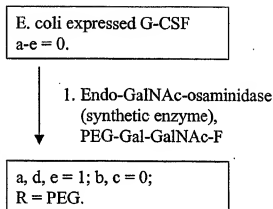


FIG. 29F

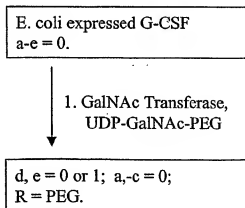
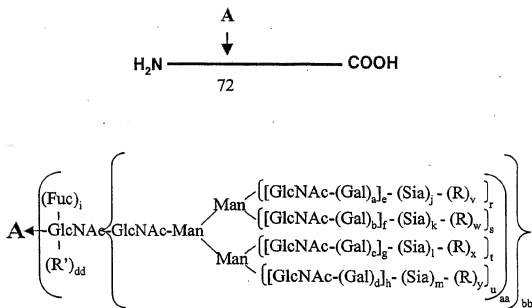


FIG. 29G

64/498



a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 30A

65/498

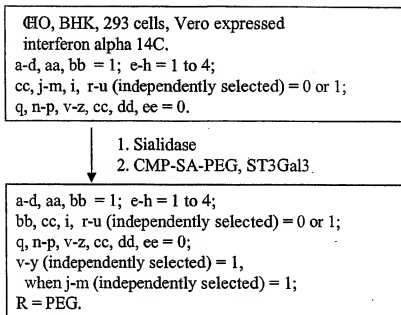


FIG. 30B

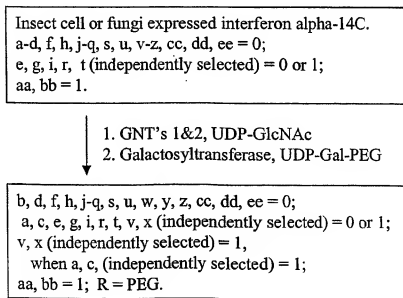


FIG. 30C

66/498

Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

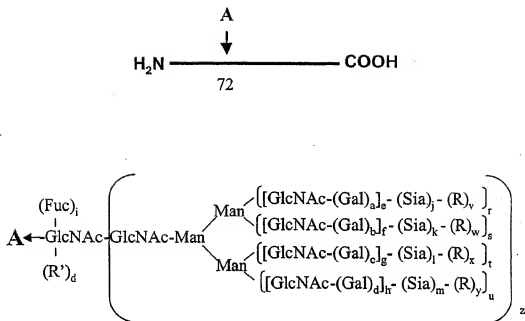
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 30D

67/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 30E

68/498

CHO, BHK, 293 cells, Vero expressed
interferon alpha-14C.

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.



1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 30F

Insect cell or fungi expressed
interferon alpha-14C.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0 or 1;

z = 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 30G

69/498

Yeast expressed interferon alpha-14C.
 a-n = 0; r-y (independently selected) = 0 to 1;
 z = 1; R (branched or linear) = Man,
 oligomannose.

1. mannosidases
2. GNT's 1,2,4,5, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal
- ▼ 4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 30H

NSO expressed interferon alpha 14C.
 a-i, r-u (independently selected) = 0 or 1;
 j-m, n, v-y = 0; z = 1.

1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
- ▼ 2. H₄N₂-PEG

a-i, j-m, r-y (independently selected) = 0 or 1;
 n = 0; z = 1; R = PEG.

FIG. 30I

70/498

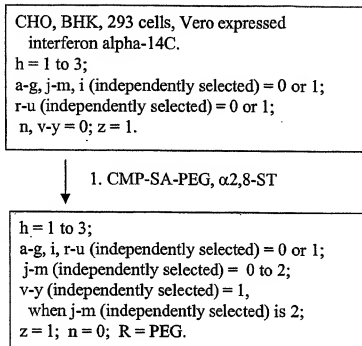


FIG. 30J

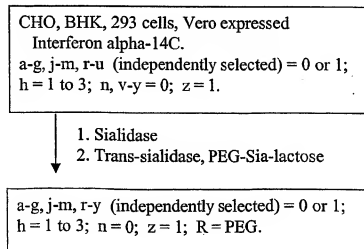


FIG. 30K

71/498

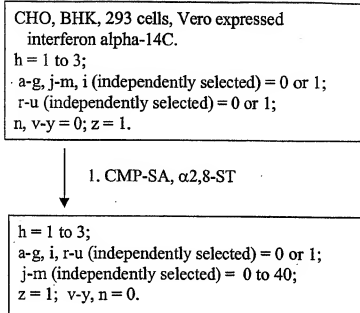


FIG. 30L

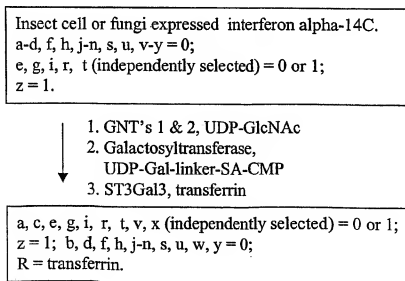


FIG. 30M

72/498

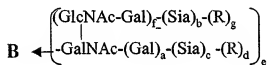
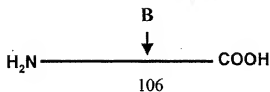
Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
 2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
 3. ST3Gal3, transferrin

i (independently selected) = 0 or 1;
a-h, j-m, r-z = 0;
n = 1; R' = -Gal-linker-transferrin.

FIG. 30N

73/498



a-c, e, f (independently selected) = 0 or 1;
 d, g = 0; R = polymer, glycoconjugate.

FIG. 300

74/498

CHO, BHK, 293 cells, Vero expressed
IF-alpha (2a or 2b).
a-c (independently selected) = 0 or 1;
e = 1; d, f, g = 0

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal1

a-d (independently selected) = 0 or 1;
e = 1; b, f, g = 0; R = PEG.

FIG. 30P

Insect cell expressed interferon alpha (2a or 2b).
a, e (independently selected) = 0 or 1;
b, c, d, f, g = 0.

- ↓
1. Galactosyltransferase, UDP-Gal
 2. CMP-SA-PEG, ST3Gal1

a, c, d, e (independently selected) = 0 or 1;
b, f, g = 0; R = PEG.

FIG. 30Q

75/498

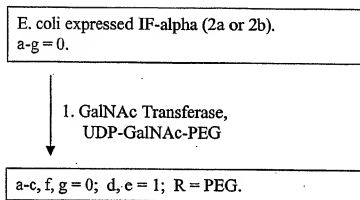


FIG. 30R

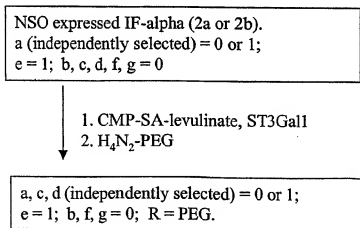


FIG. 30S

76/498

E. coli expressed IF-alpha (2a or 2b).
a-g = 0.



1. Endo-N-acetylgalactosamidase
(synthetic enzyme),
PEG-Gal-GalNAc-F

a, d, e = 1; b, c, f, g = 0; R = PEG.

FIG. 30T

E. coli expressed IF-alpha (2a or 2b).
a-g = 0.



1. GalNAc Transferase, UDP-GalNAc
2. sialyltransferase, CMP-SA-PEG

b, d = 0 or 1; e = 1; a, c, f, g = 0; R = PEG.

FIG. 30U

77/498

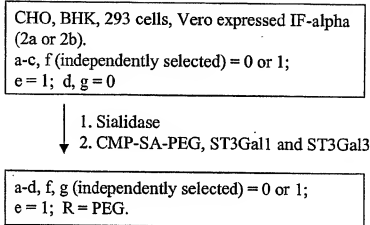


FIG. 30V

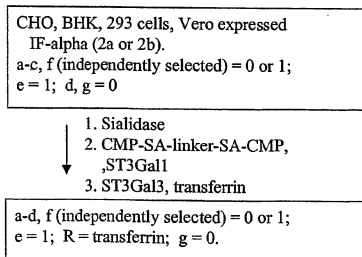
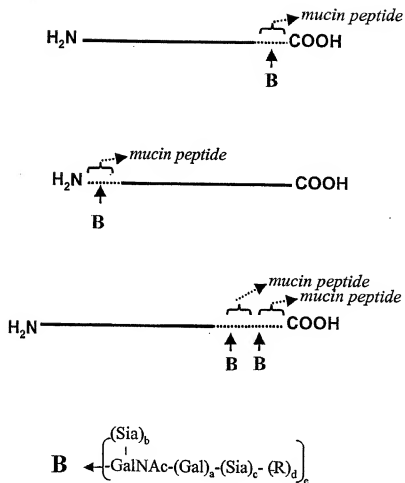


FIG. 30W

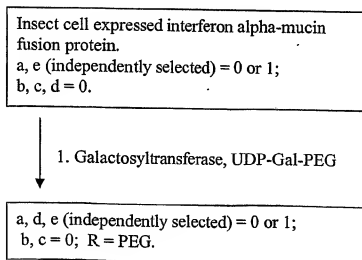
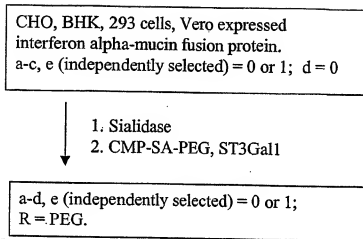
78/498



a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer, glycoconjugate.

FIG. 30X

79/498



80/498

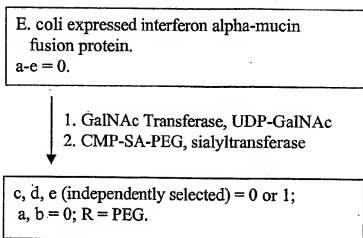
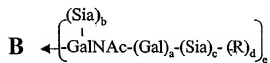
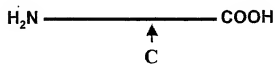
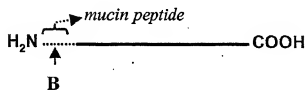
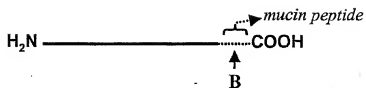


FIG. 30AA

81/498



a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 30BB

82/498

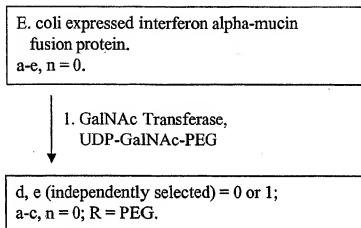


FIG. 30CC

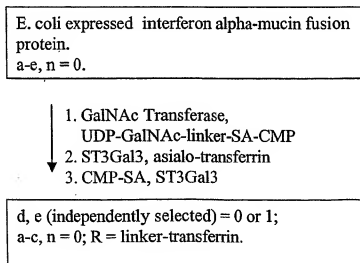


FIG. 30DD

83/498

E. coli expressed Interferon alpha (no fusion).
a-e, n = 0.

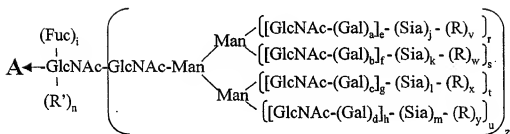
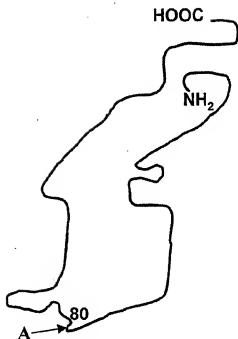


1. NHS-CO-linker-SA-CMP
2. ST3Gal3, transferrin

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 30EE

84/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 31A

85/498

CHO, BHK, 293 cells, Vero expressed IF-beta
 h = 1 to 3;
 a-g, j-m, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;
 a-g, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 31B

Insect cell expressed IF-beta
 a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, r, t (independently selected) = 0 or 1;
 z = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3,
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 j, l, v, x (independently selected) = 0 or 1;
 z = 1; R = PEG.

FIG. 31C

86/498

Yeast expressed IF-beta
 a-n = 0; z = 1;
 r-y (independently selected) = 0 to 1;
 R (branched or linear) = Man, oligomannose or
 polysaccharide.

- ↓ 1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed IF-beta
 h = 1 to 3;
 a-g, j-m, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1.

- ↓ 1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;
 a-g, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 31E

87/498

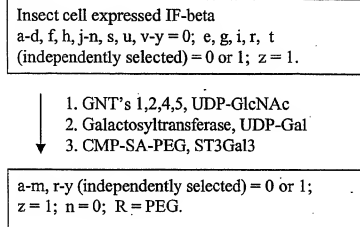


FIG. 31F

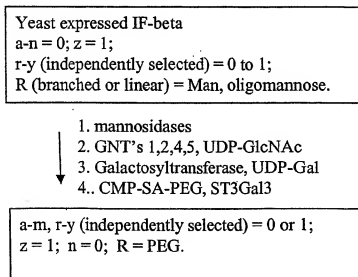


FIG. 31G

88/498

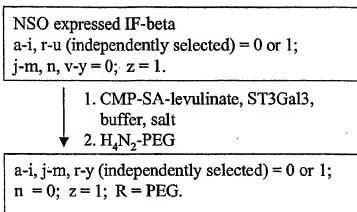


FIG. 31H

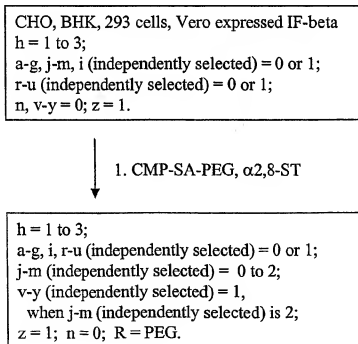


FIG. 31I

89/498

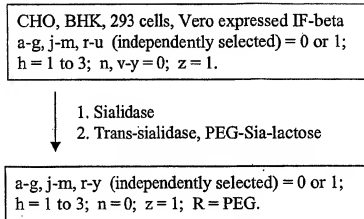


FIG. 31J

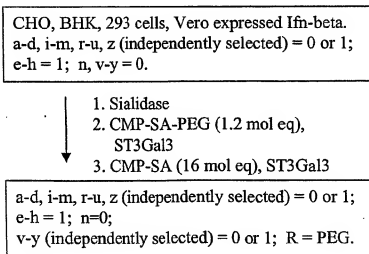


FIG. 31K

90/498

NSO expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; R = PEG

n = 0; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

FIG. 31L

CHO, BHK, 293 cells, Vero expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n = 0;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 31M

91/498

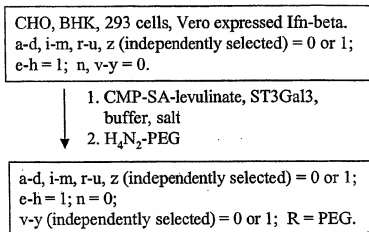


FIG. 31N

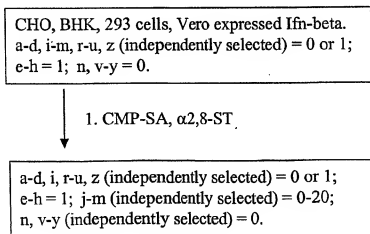
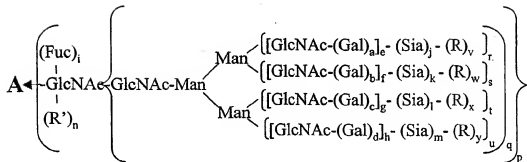
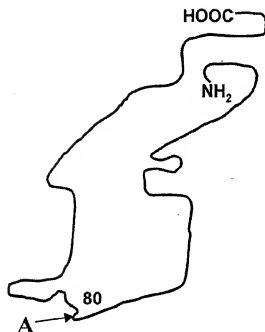


FIG. 31O

92/498



a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group;

R' = H, glycosyl group, modifying group,

glycoconjugate.

FIG. 31P

93/498

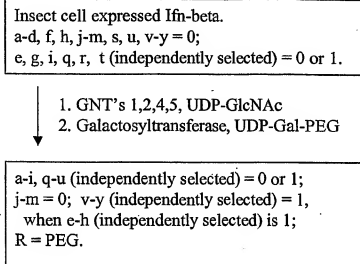


FIG. 31Q

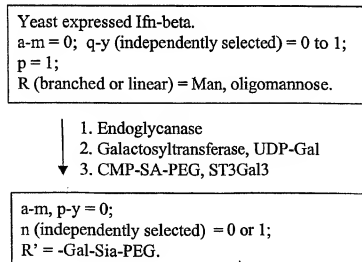


FIG. 31R

94/498

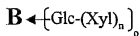
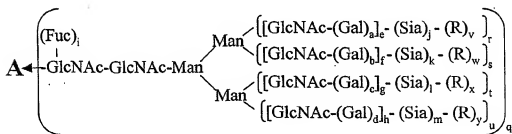
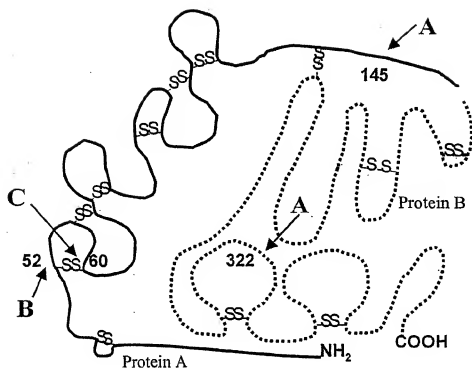
CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 31S

95/498



a-d, i, q-u (independently selected) = 0 or 1.

 o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

$$v - y = 0;$$

R = modifying group, mannose, oligomannose, Sia-Lewis X, Sia-Lewis A..

FIG. 32A

96/498

BHK expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mole eq),
ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
v, x, (independently selected) = 1,
when j, l (respectively, independently selected) is 1;
R = PEG.

FIG. 32B

CHO, BHK, 293 cells, Vero expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mole eq),
ST3Gal3
 3. CMP-SA (8 mol eq), ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
v or x, (independently selected) = 1,
when j or l, (respectively, independently selected) is 1;
R = PEG.

FIG. 32C

97/498

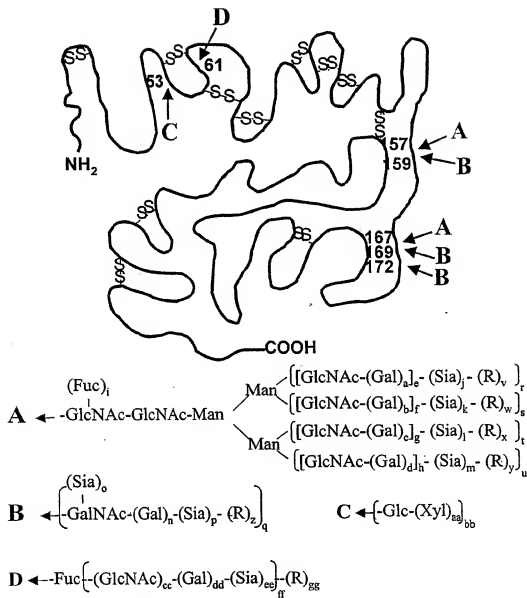
NSO expressed Factor VII or VIIa
a--u (independently selected) = 0 or 1;
v-y = 0; n = 0-4;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;
n = 0-4; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
Sia = Sia; R = PEG.

FIG. 32D

98/498



a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 33A

99/498

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 R = PEG.

FIG. 33B

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3
 3. ST3Gal1, CMP-SA

a-d, n, p, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 o, z = 0; R = PEG.

FIG. 33C

100/498

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

- ↓
1. sialidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA, ST3Gal3
 4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1; R = PEG;
 o, v-y, gg = 0;
 j-m, p, ee (independently selected) = 0 or 1, but when
 p = 1, z = 1.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
- CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1; R = PEG;
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =
 0 or 1.

FIG. 33E

101/498

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 33F

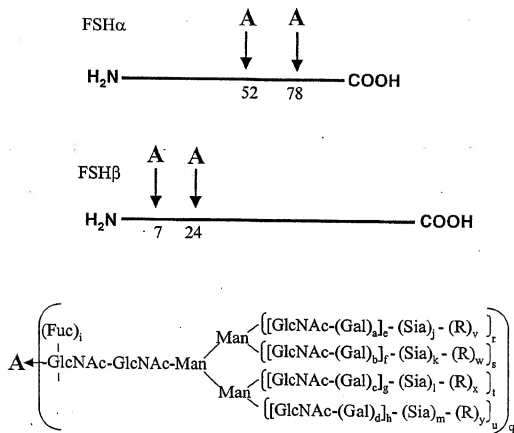
CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1;
 e-h, aa = 1 to 4;
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG, α 2,8-ST

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee (independently selected) = 0 to 2;
 v-y, gg (independently selected) = 1, when j-m
 (independently selected) is 2;

FIG. 33G

102/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 34A

103/498

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 34B

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 34C

104/498

NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 34D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 34E

105/498

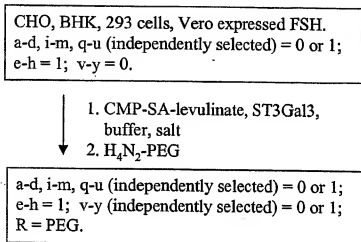


FIG. 34F

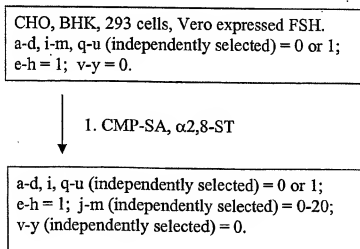


FIG. 34G

106/498

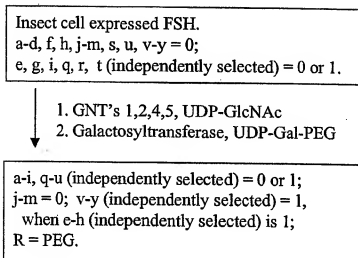


FIG. 34H

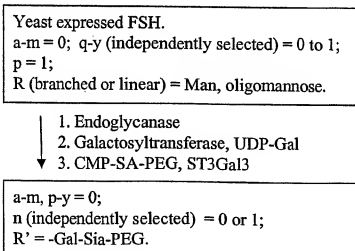


FIG. 34I

107/498

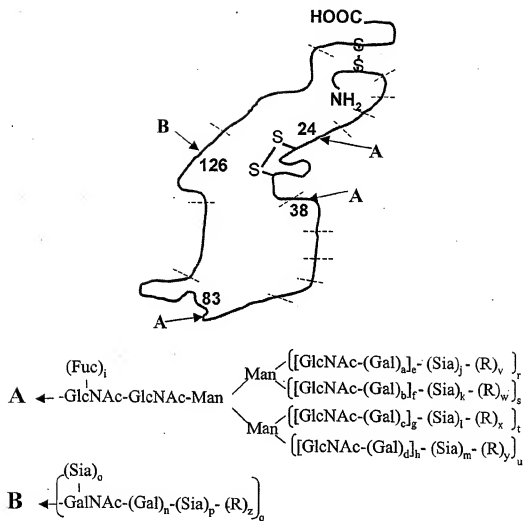
CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated chorionic gonadotrophin (CG) produced in CHO.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-CG.

FIG. 34J

108/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35A

109/498

CHO, BHK, 293 cells, Vero expressed EPO
 a-g, n, q = 1; h = 1 to 3;
 j-m, i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1; v-z = 0

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;
 i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 R = PEG; z = 0.

FIG. 35B

Insect cell expressed EPO
 a-d, f, h, j-q, s, u, v-z = 0;
 e, g, i, r, t (independently selected) = 0 or 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal
 2. CMP-SA-PEG, ST3Gal3

b, d, f, h, k, m-q, s, u, w, y, z = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 j, l, v, x (independently selected) = 0 or 1;
 R = PEG.

FIG. 35C

110/498

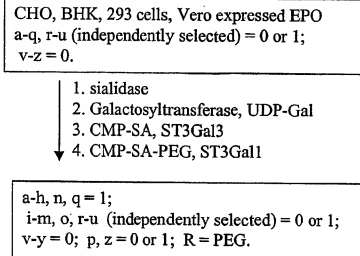


FIG. 35D

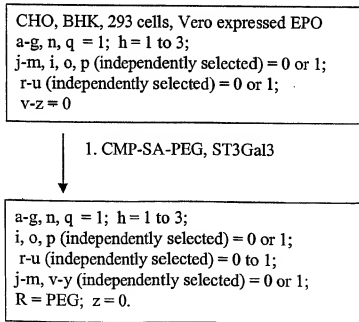


FIG. 35E

111/498

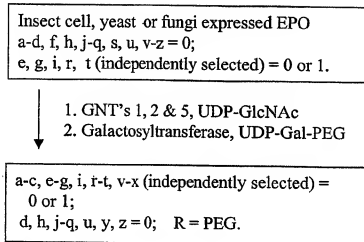


FIG. 35F

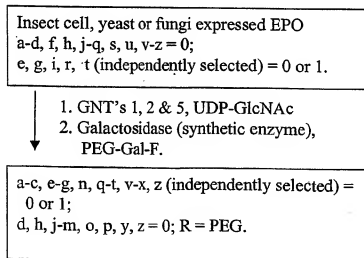


FIG. 35G

112/498

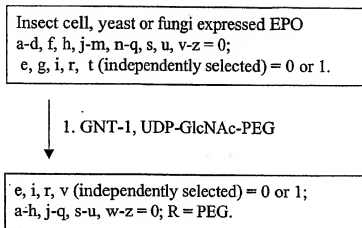


FIG. 35H

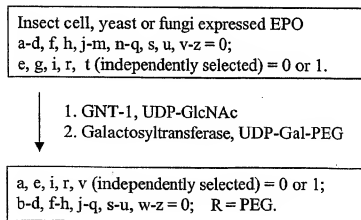


FIG. 35I

113/498

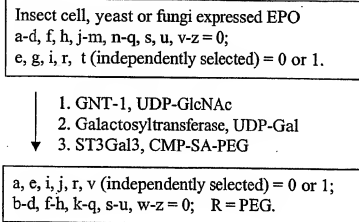


FIG. 35J

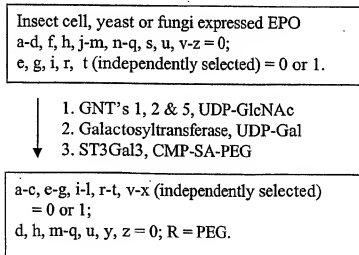


FIG. 35K

114/498

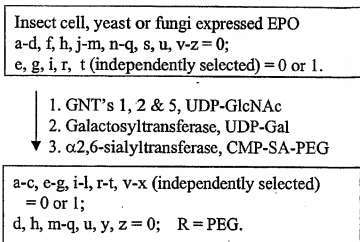


FIG. 35L

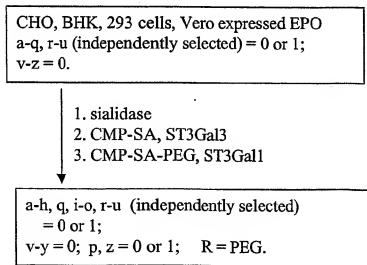


FIG. 35M

115/498

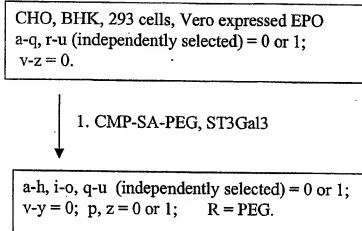


FIG. 35N

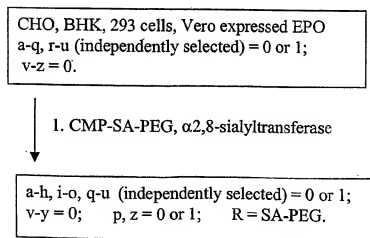


FIG. 35O

116/498

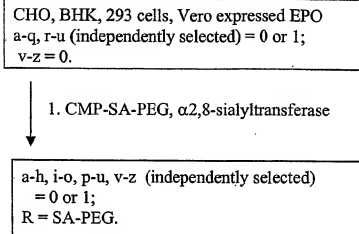


FIG. 35P

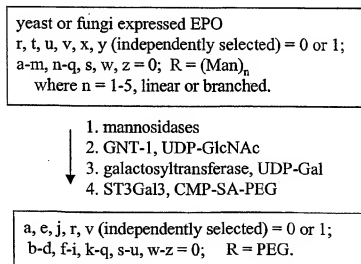


FIG. 35Q

117/498

yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 a-m, n-q, s, w, z = 0; $R = (\text{Man})_n$
 where n = 1-5, linear or branched.

- ↓
1. mannosidases
 2. GNT-1, UDP-GlcNAc-PEG

c, r, v (independently selected) = 0 or 1;
 a-h, i-q, s-u, w-z = 0; $R = \text{PEG}$.

FIG. 35R

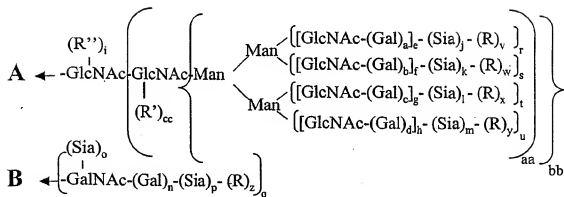
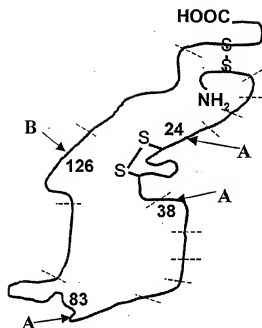
yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 a-m, n-q, s, w, z = 0; $R = (\text{Man})_n$
 where n = 1-5, linear or branched.

- ↓
1. mannosidase-I
 2. GNT-1, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal
 4. ST3Gal3, CMP-SA-PEG

a, c, j, r, t-u, v, x, y (independently selected)
 = 0 or 1;
 b-d, f-i, k-q, s, w, z = 0;
 $(R)_v = \text{PEG}$; $(R)_x$ and $(R)_y = \text{Man}$.

FIG. 35S

118/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; aa, bb = 1; cc = 0;

R = polymer; R'' and R' = sugar-polymer or Fuc.

FIG. 35T

119/498

yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 cc, a-m, n-q, s, w, z = 0;
 aa, bb = 1;
 $R = (\text{Man})_n$ where $n = 1-100$, linear or branched.

- ↓
 1. endo-H
 2. galactosyltransferase, UDP-Gal-PEG

i (independently selected) = 0 or 1;
 aa, bb, cc, a-h, j-z = 0; $R'' = \text{Gal-PEG}$.

FIG. 35U

yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 cc, a-m, n-q, s, w, z = 0; aa, bb = 1;
 $R = (\text{Man})_n$ where $n = 1-100$, linear or branched.

- ↓
 1. endo-H
 2. galactosyltransferase, UDP-Gal
 3. ST3Gal3, CMP-SA-PEG

i (independently selected) = 0 or 1;
 aa, bb, cc, a-h, j-z = 0; $R'' = \text{Gal-SA-PEG}$.

FIG. 35V

120/498

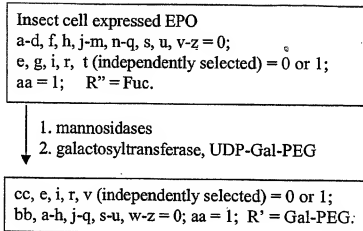


FIG. 35W

122/498

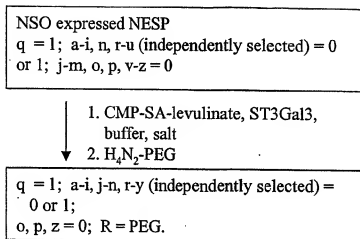


FIG. 35Y

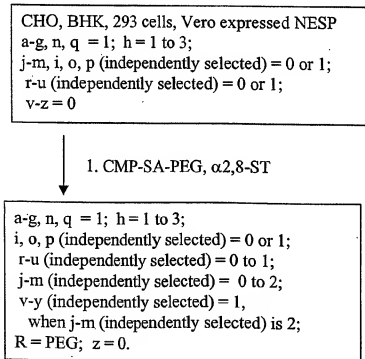


FIG. 35Z

123/498

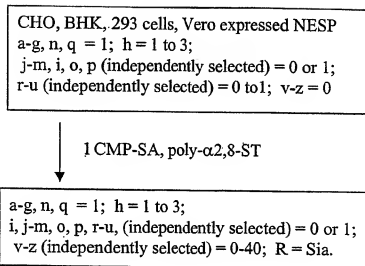
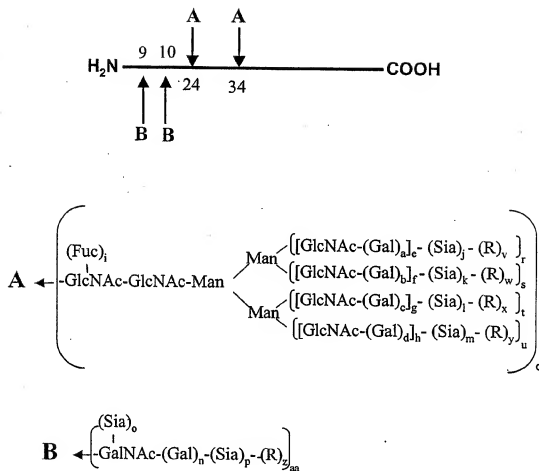


FIG. 35AA

124/498



a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 36A

125/498

CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
 o, p, z = 0; n, e-h = 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 36B

CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3 &
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;
 o, z = 0; n, e-h = 1;
 v-y (independently selected) = 0 or 1; R = PEG.

FIG. 36C

126/498

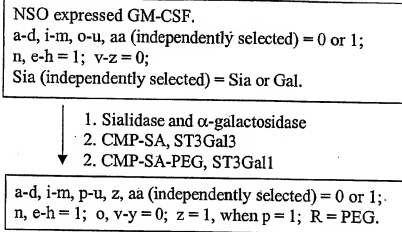


FIG. 36D

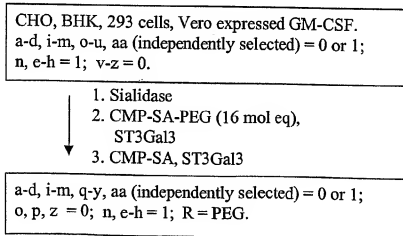


FIG. 36E

127/498

CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;
z = 0; n, e-h = 1; R = PEG.

FIG. 36F

CHO, BHK, 293 cells, Vero expressed GMCSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

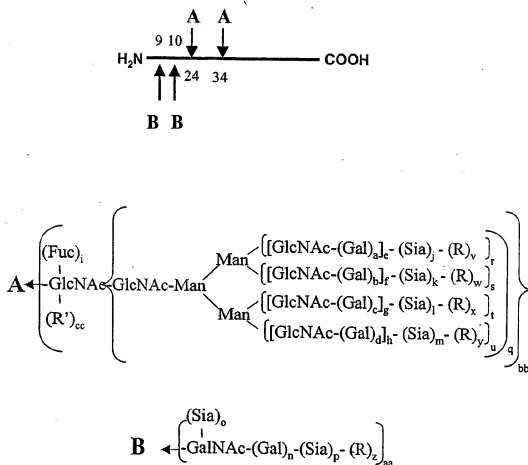


1. CMP-SA, α 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; j-m (independently selected) = 0-20;
v-z (independently selected) = 0.

FIG. 36G

128/498



a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

c-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 36H

129/498

Insect cell expressed GM-CSF.

a-d, f, h, j-m, o, p, s, u, v-z = 0;

c, g, i, n, q, r, t, aa (independently selected) = 0 or 1.

1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, n, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 36I

Yeast expressed GM-CSF.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1;

bb = 1; R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. Endoglycanase
2. mannosidase (if aa = 1).
3. Galactosyltransferase, UDP-Gal-PEG

a-p, r-z, aa, bb = 0;

q, cc (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 36J

130/498

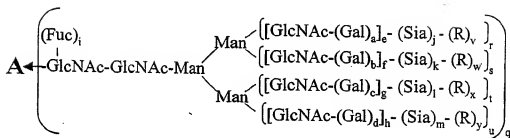
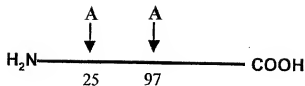
CHO, BHK, 293 cells, Vero expressed GM-CSF.
a--m, o-u, aa, bb (independently selected) = 0 or 1;
n, v-z, cc = 0.

- ↓
1. sialidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-linker-SA-CMP, ST3Gal1
 3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 36K

131/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 37A

132/498

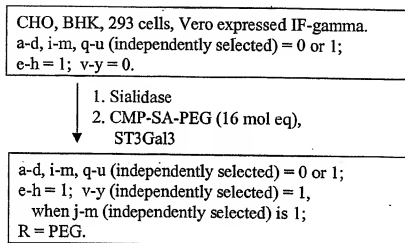


FIG. 37B

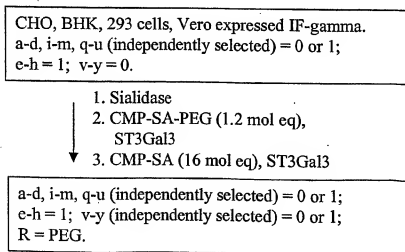


FIG. 37C

133/498

NSO expressed Interferon gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 37D

CHO, BHK, 293 cells, Vero expressed
Interferon gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 37E

134/498

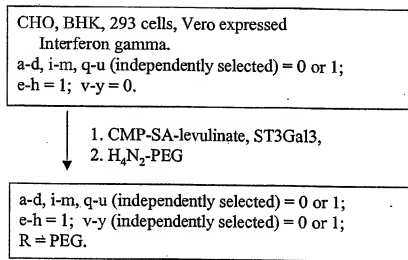


FIG. 37F

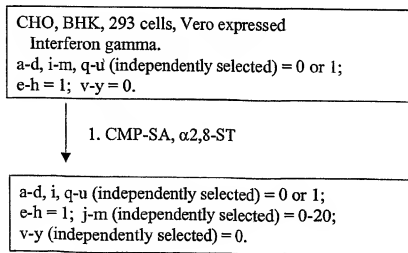
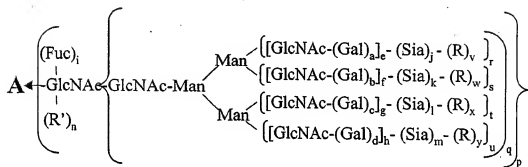
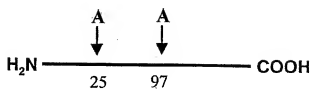


FIG. 37G

135/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 37H

136/498

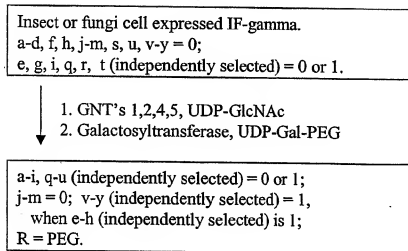


FIG. 37I

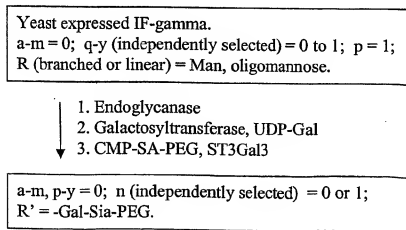


FIG. 37J

137/498

CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP, ST3Gal3
 2. Galactosyltransferase, transferrin treated with endoglycanase.

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 37K

CHO, BHK, 293 cells, Vero expressed
Interferon gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1; n, v-y = 0.

- ↓
1. CMP-SA-PEG,
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1;
n, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 37L

138/498

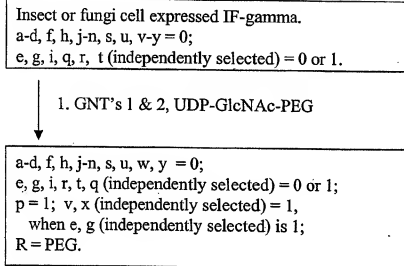


FIG. 37M

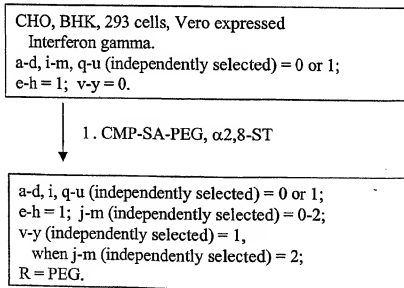
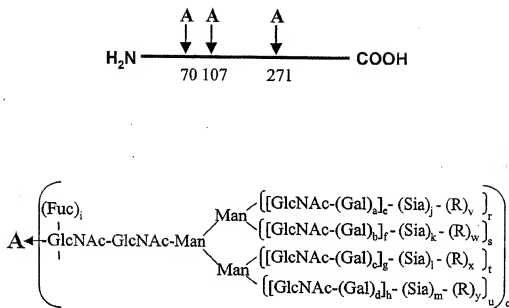


FIG. 37N

139/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 38A

140/498

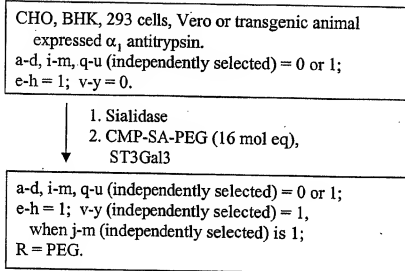


FIG. 38B

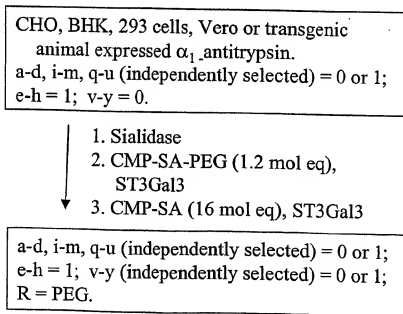


FIG. 38C

141/498

CHO, BHK, 293 cells, Vero or transgenic animal
expressed alpha-1 antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38D

CHO, BHK, 293 cells, Vero or transgenic animal
expressed α_1 -antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38E

142/498

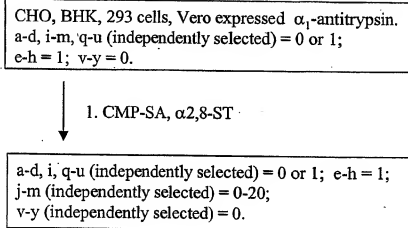
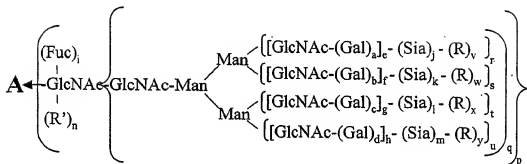
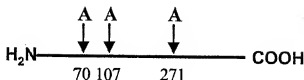


FIG. 38F

143/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 38G

144/498

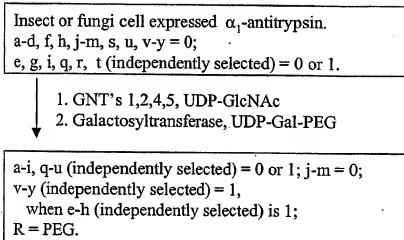


FIG. 38H

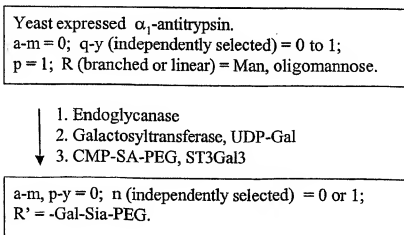


FIG. 38I

145/498

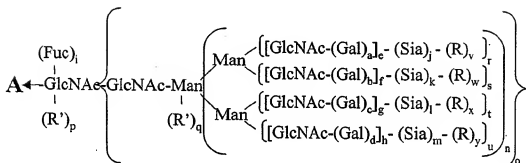
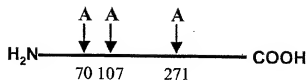
CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin treated
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 38J

146/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 38K

147/498

Yeast expressed alpha-1 antitrypsin.

a-h, i-m, p, q = 0;

R (independently selected) = mannose, oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1; n, o = 1.

↓ 1. endoglycanase

▼ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R'' = Gal-PEG.

FIG. 38L

Plant expressed alpha-1 antitrypsin.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1;

n = 1; R' = xylose

↓ 1. hexosaminidase,

2. alpha mannosidase and xylosidase

▼ 3. GlcNAc transferase, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0;

q = 1; R' = GlcNAc-PEG.

FIG. 38M

148/498

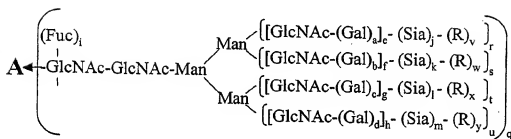
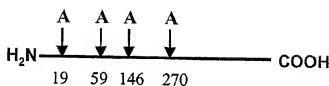
CHO, BHK, 293 cells, Vero, transgenic animal
expressed α_1 antitrypsin.
a-h, i-o, r-u (independently selected) = 0 or 1;
p, q, v-y = 0.

↓
1. CMP-SA-PEG,
ST3Gal3

a-h, i-o, r-u (independently selected) = 0 or 1;
p, q = 0; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38N

149/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

$$v-y=0; \quad R = \text{polymer.}$$

FIG. 39A

150/498

CHO, BHK, 293 cells, Vero expressed Cerezyme
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 39B

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-M-6-P (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = mannose-6-phosphate

FIG. 39C

151/498

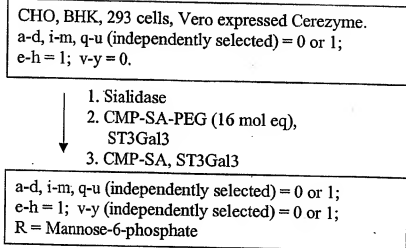


FIG. 39D

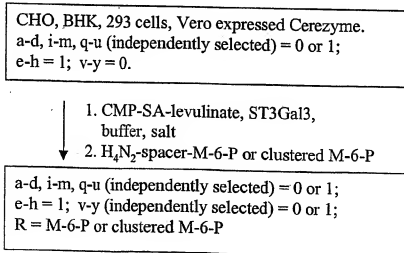


FIG. 39E

152/498

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 39F

153/498

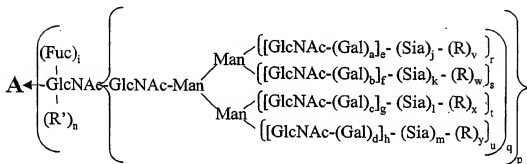
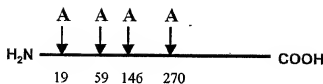


FIG. 39G

154/498

Insect cell expressed Cerezyme.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 39H

Yeast expressed Cerezyme.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 39I

155/498

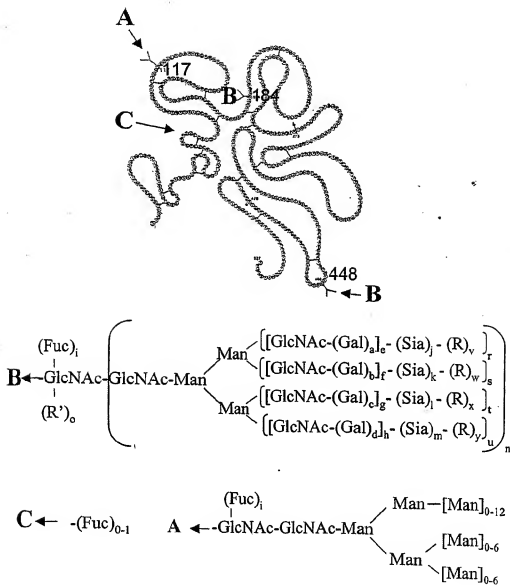
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0; v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 39J

156/498



a-d, i, n-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 4.
 j-m (independently selected) = 0 to 20.
 R = polymer; R' = sugar, glycoconjugate.

FIG. 40A

157/498

CHO, BHK, 293 cells, Vero expressed tPA
 a-g, n = 1; h = 1 to 3;
 j-m, i, (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
- ▼ 4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;
 i, r-u (independently selected) = 0 or 1;
 o = 0; j-m, v-y (independently selected) = 0 or 1;
 R = PEG

FIG. 40B

Insect or fungi cell expressed tPA
 A = B; a-d, f, h, j-o, s, u, v-y = 0;
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
- ▼ 3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 n = 1; j, l, v, x (independently selected) = 0 or 1;
 R = PEG.

FIG. 40C

158/498

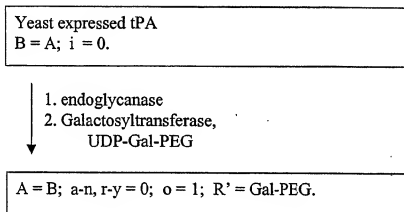


FIG. 40D

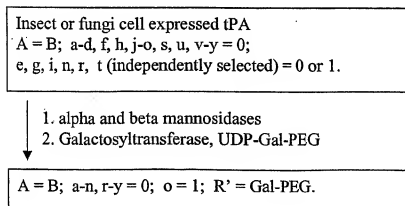


FIG. 40E

159/498

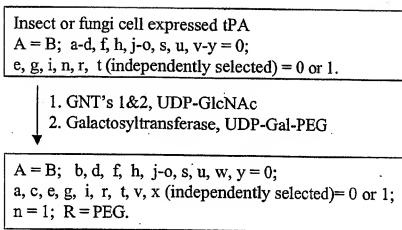


FIG. 40F

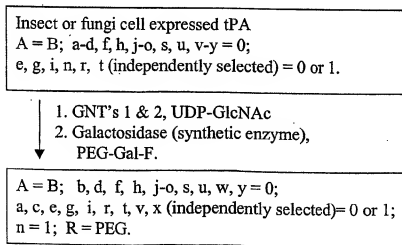
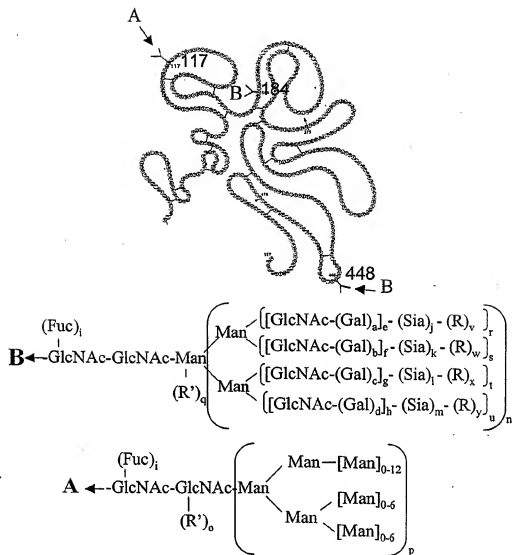


FIG. 40G

160/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40H

161/498

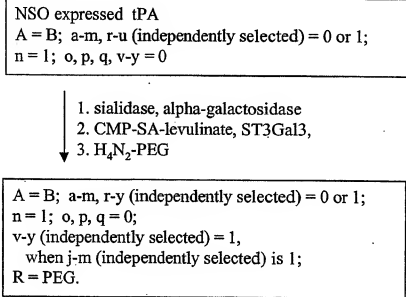


FIG. 40I

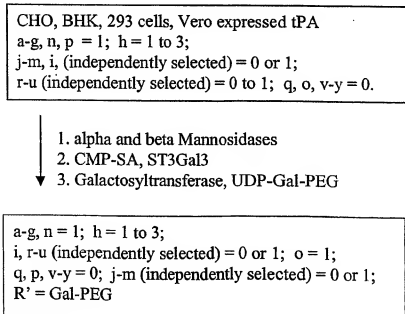


FIG. 40J

162/498

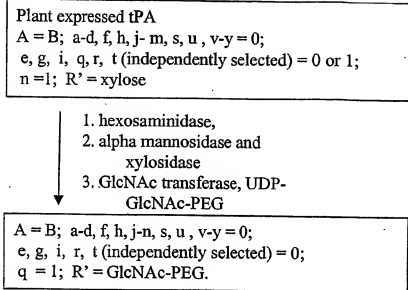


FIG. 40K

164/498

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 40M

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40N

165/498

NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

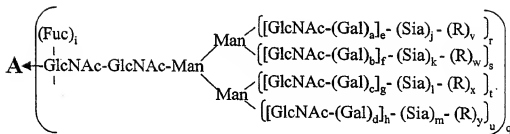
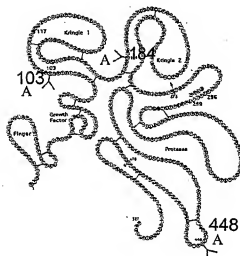
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 400

166/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40P

167/498

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40Q

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40R

168/498

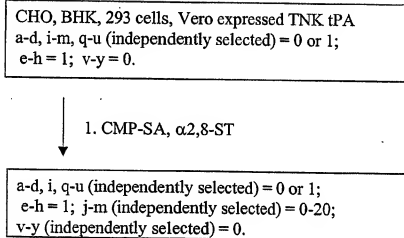
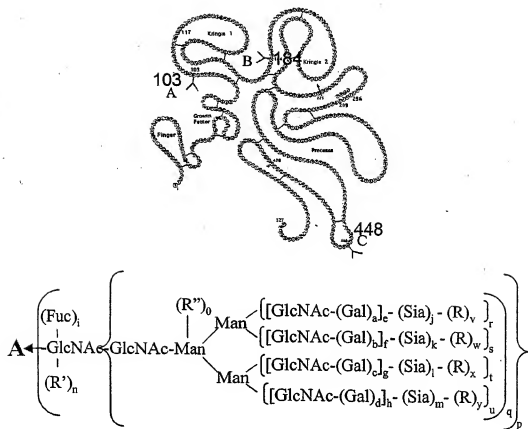


FIG. 40S

169/498



a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 40T

170/498

Insect cell expressed TNK tPA

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 40U

Yeast expressed TNK tPA

a-m = 0; q-y (independently selected) = 0 to 1; p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal-PEG

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 40V

171/498

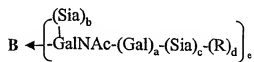
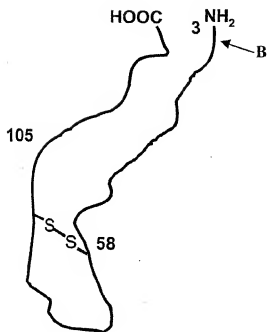
CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, anti-TNF
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;
n = 0; v-y (independently selected) = 0 or 1;
R = linker-anti-TNF IG chimera protein.

FIG. 40W

172/498



a-c, e (independently selected) = 0 or 1;
 d = 0;
 R = modifying group, mannose, oligo-
 mannose.

FIG. 41A

173/498

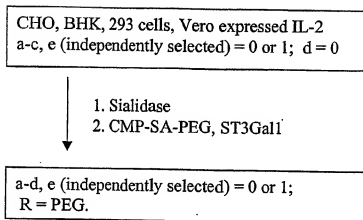


FIG. 41B

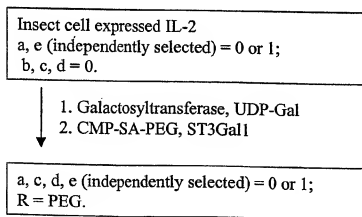


FIG. 41C

174/498

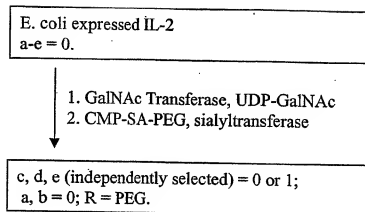


FIG. 41D

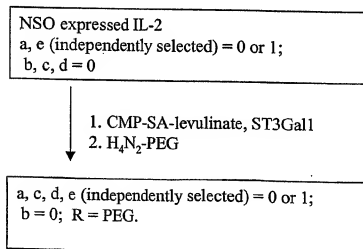


FIG. 41E

175/498

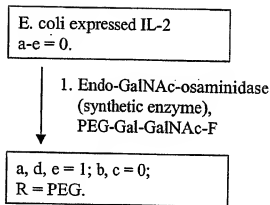


FIG. 41F

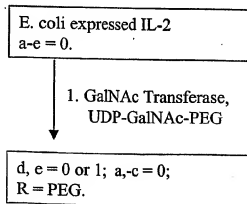


FIG. 41G

177/498

CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
2. CMP-SA-PEG, ST3Gal3
3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42C

178/498

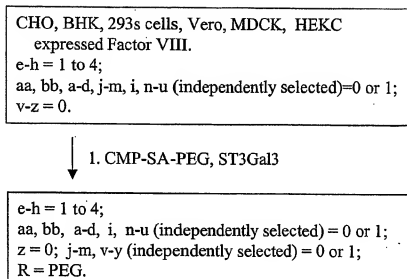


FIG. 42D

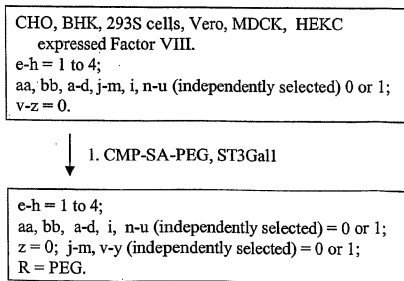


FIG. 42E

179/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;
v-z = 0.



1. CMP-SA-PEG, α 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

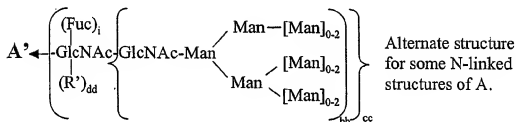
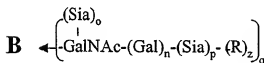
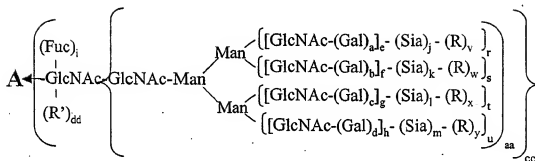
when j-m (independently selected) is 2;

R = PEG.

FIG. 42F

180/498

2 peptides

A or A' - N-linked sites**B** - O-linked sites

a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 42G

181/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
 2. H₄N₂-PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;
dd, z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42H

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. endo-H
 2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;
cc, v-z = 0; R' = -Gal-PEG.

FIG. 42I

182/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
 2. endo-H
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;
cc, v-z = 0; R' = -Gal-PEG.

FIG. 42J

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT 1 & 2, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;
bb, cc, dd, z = 0; R = PEG.

FIG. 42K

183/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT-1, 2, 4 & 5; UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal
 4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;
dd, v-z = 0.

FIG. 42L

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT-1, UDP-GlcNAc-PEG

e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;
bb, cc, dd, z = 0.

FIG. 42M

185/498

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 43B

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 43C

186/498

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 43D

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 43E

187/498

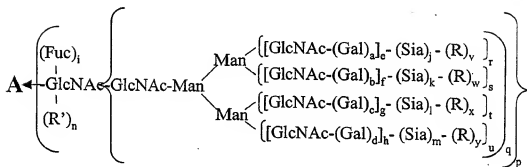
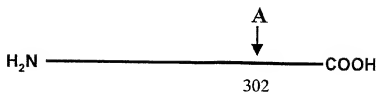
CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 43F

188/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 43G

189/498

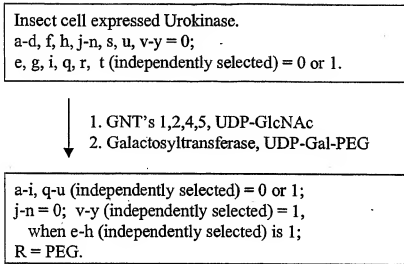


FIG. 43H

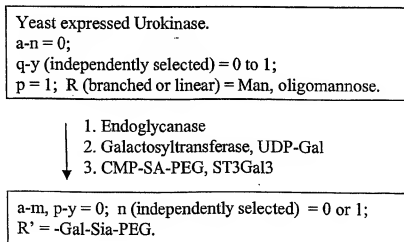


FIG. 43I

190/498

CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated Urokinase produced in CHO.
 - ↓ 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;

p = 1; n = 0;

v-y (independently selected) = 0 or 1;

R = linker-Urokinase.

FIG. 43J

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0; n = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase
 2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

n = 0; e-h = 1; Sia = Sia;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 43K

191/498

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase, hexosaminidase
 2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

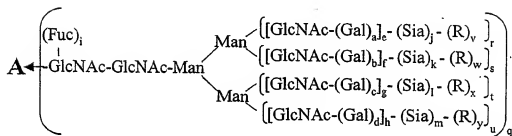
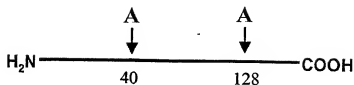
e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 43L

192/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

193/498

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 44C

194/498

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq), ST3Gal3
3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 44D

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 44E

195/498

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 44F

197/498

Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 44H

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 44I

198/498

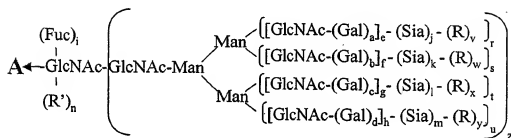
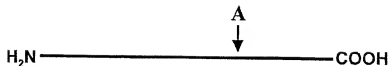
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker- alpha-1-Proteinase inhibitor.

FIG. 44J

199/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 45A

200/498

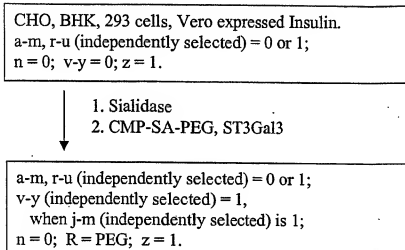


FIG. 45B

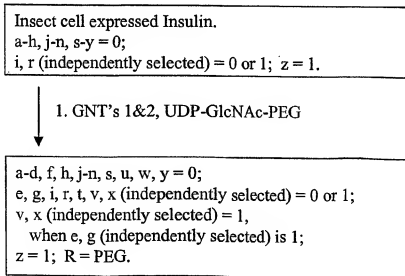


FIG. 45C

201/498

Yeast expressed Insulin.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.



1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 45D

203/498

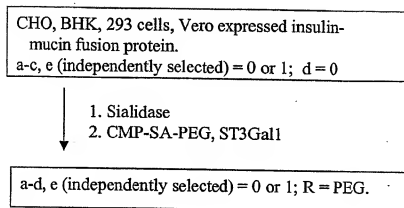


FIG. 45F

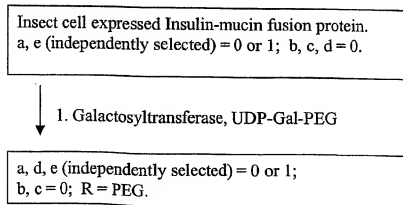


FIG. 45G

204/498

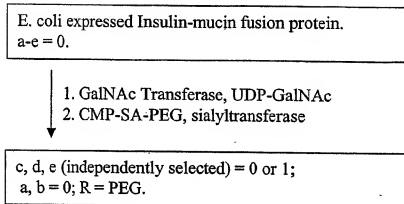
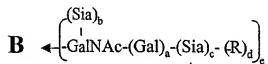
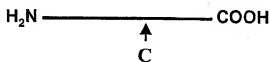
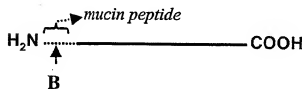
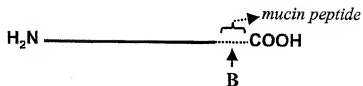


FIG. 45H

205/498



a-c, e (independently selected) = 0 or 1;
 d = 0; R = modifying group, mannose,
 oligo-mannose.

FIG. 45I

206/498

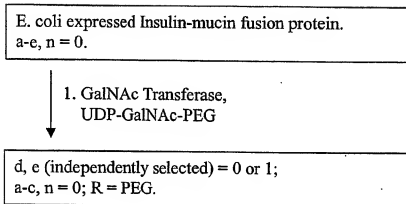


FIG. 45J

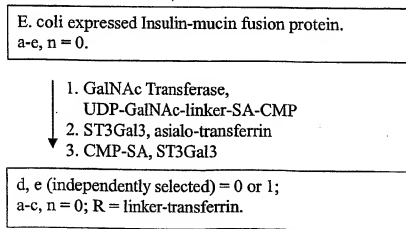


FIG. 45K

207/498

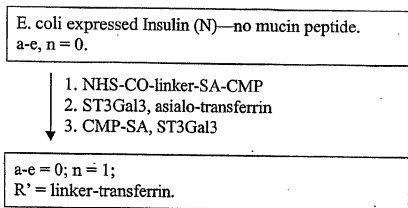
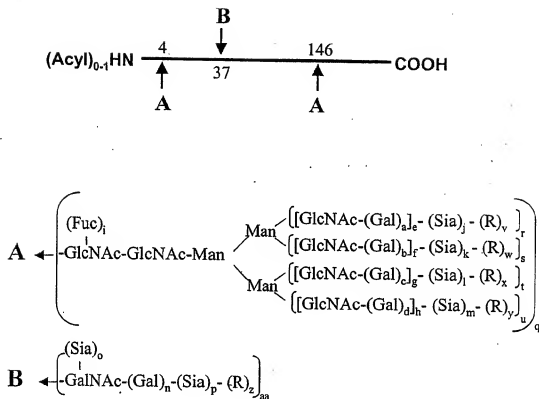


FIG. 45L

208/498



a-d, i, n-u, aa (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer, glycoconjugate.

FIG. 46A

209/498

CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-linker-lipid-A,
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
o, p, z = 0; n, e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = linker-lipid-A.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-linker-tetanus toxin, ST3Gal1
 3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 46C

210/498

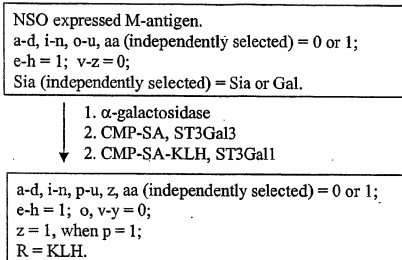


FIG. 46D

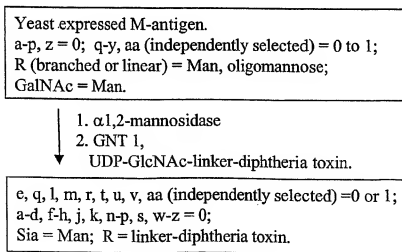


FIG. 46E

211/498

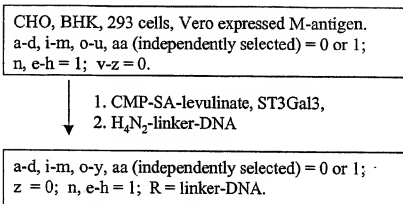


FIG. 46F

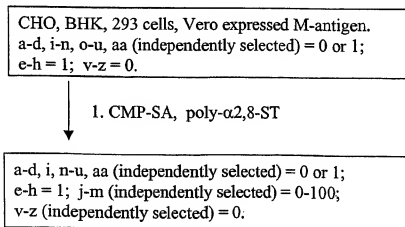
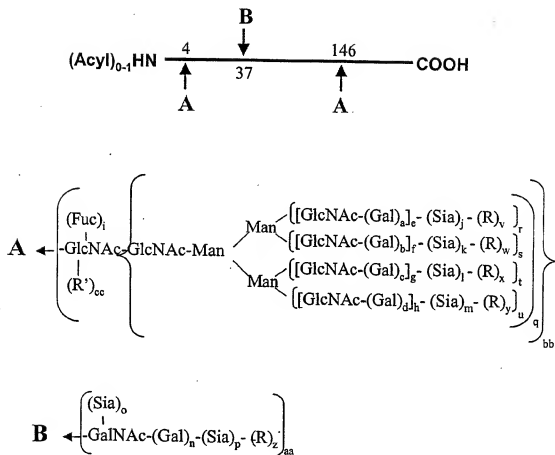


FIG. 46G

212/498



a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46H

213/498

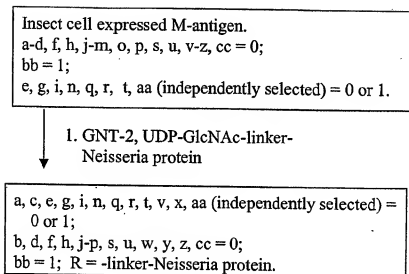


FIG. 46I

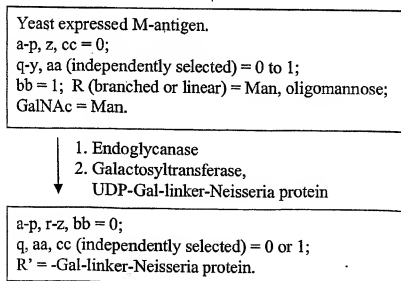


FIG. 46J

214/498

Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. mannosidases

2. GNT 1 & 2, UDP-GlcNAc

3. UDP-Gal, Galactosyltransferase,

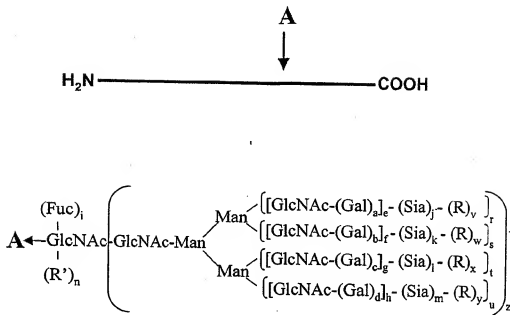
4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;

b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 46K

215/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 47A

216/498

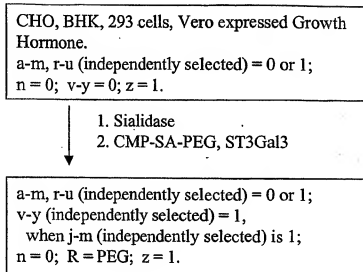


FIG. 47B

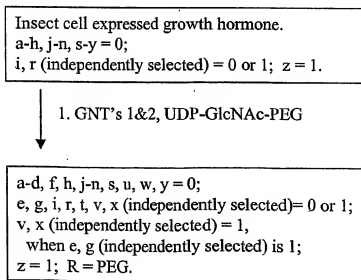


FIG. 47C

217/498

Yeast expressed growth hormone.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

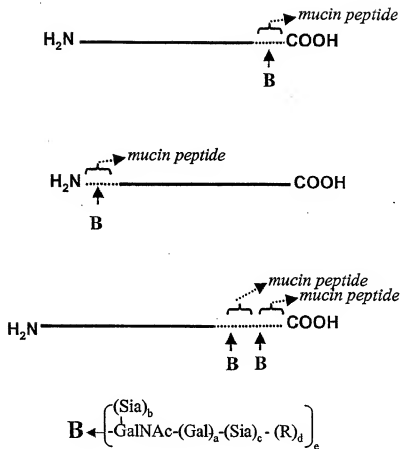
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 47D

218/498



a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 47E

219/498

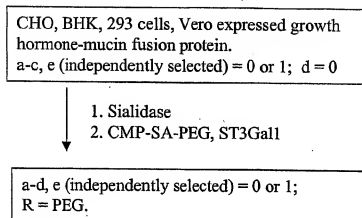


FIG. 47F

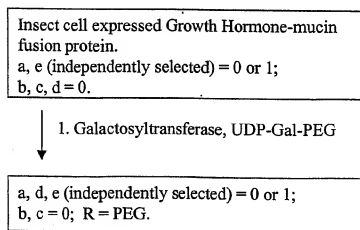


FIG. 47G

220/498

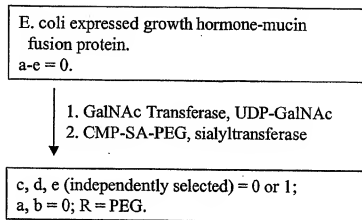


FIG. 47H

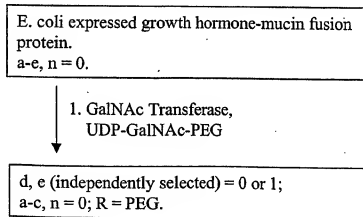


FIG. 47I

221/498

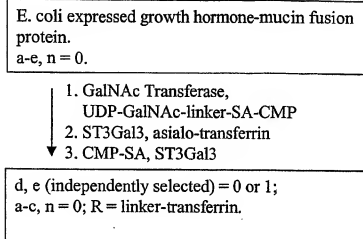


FIG. 47J

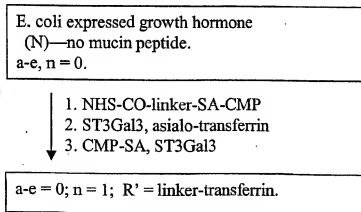
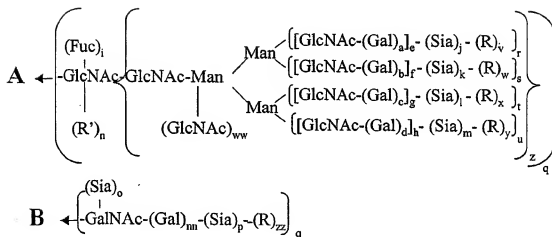
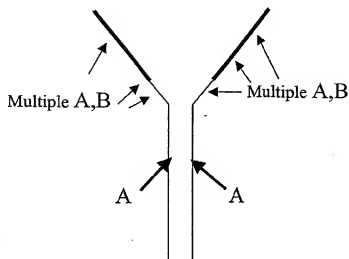


FIG. 47K

222/498



a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

223/498

CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
 2. galactosyltransferase, UPD-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 48C

224/498

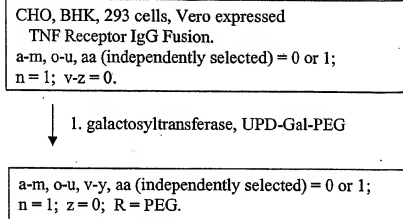


FIG. 48D

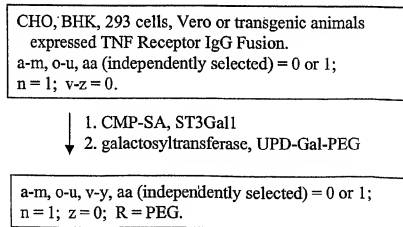


FIG. 48E

225/498

CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal1
2. H₄N₂-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48F

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.

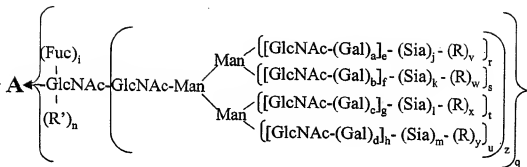
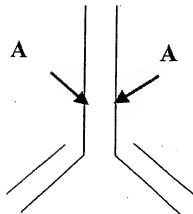
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA-PEG, α 2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;
n = 1; j-m, p (independently selected) = 0 to 2;
v-z (independently selected) = 1,
when j-m, p (independently selected) is 2;
R = PEG.

FIG. 48G

226/498



a-d, i, l, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-k (independently selected) = 0 or 1.

M = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

227/498

CHO, BHK, 293 cells, Vero expressed Herceptin.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.

- ↓
1. galactosyltransferase, UPD-Gal
 2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
 e, g, r, t = 1; R = toxin;
 f, h, k, m, n, s, u-y = 0; q, z = 1;
 v-y (independently selected) = 51,
 when j, l (independently selected) is 1.

FIG. 49B

CHO, BHK, 293 cells, Vero or fungal expressed Herceptin.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.

- ↓
1. galactosyltransferase,
UPD-Gal-Toxin

a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when a, c (independently selected) is 1;
 R = toxin.

FIG. 49C

228/498

Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

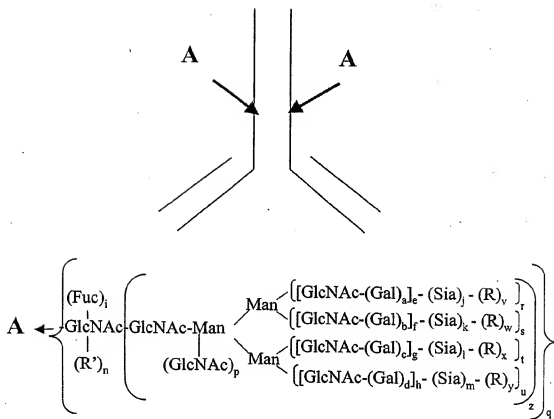
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D

229/498



a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 50A

230/498

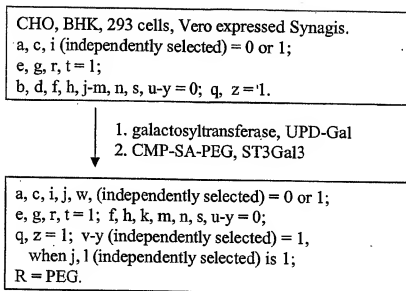


FIG. 50B

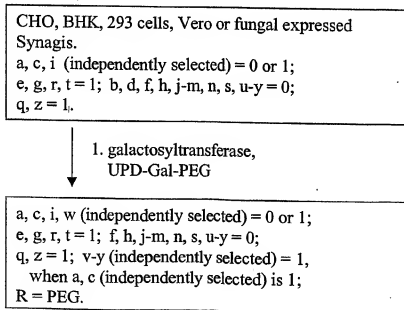


FIG. 50C

231/498

Fungi expressed Synagis.
e, g, i, r, t (independently selected) = 0 or 1;
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H
2. Galactosyltransferase, UDP-Gal
- ▼ 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 50D

233/498

CHO, BHK, 293 cells, Vero expressed Remicade.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when j, l (independently selected) is 1;
R = PEG.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed Remicade.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.



1. galactosyltransferase,
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when a, c (independently selected) is 1;
R = PEG.

FIG. 51C

234/498

Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

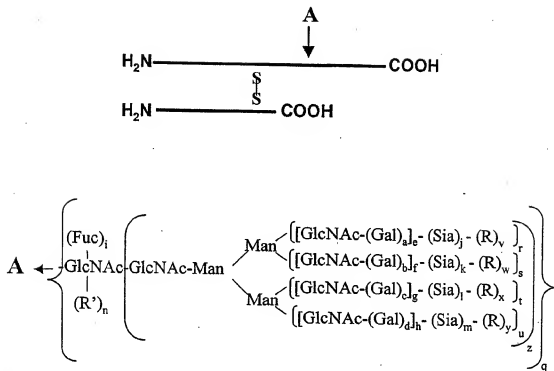
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

235/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 52A

236/498

CHO, BHK, 293 cells, Vero expressed Reopro.
a-m, r-u (independently selected) = 0 or 1;
n = 0; v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
n = 0; R = PEG; z = 1.

FIG. 52B

Insect cell expressed Reopro.
a-h, j-n, s-y = 0; i, r (independently selected) = 0 or 1;
z = 1.



1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;
e, g, i, r, t, v, x (independently selected) = 0 or 1;
v, x (independently selected) = 1,
when e, g (independently selected) is 1;
z = 1; R = PEG.

FIG. 52C

237/498

Yeast expressed Reopro.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

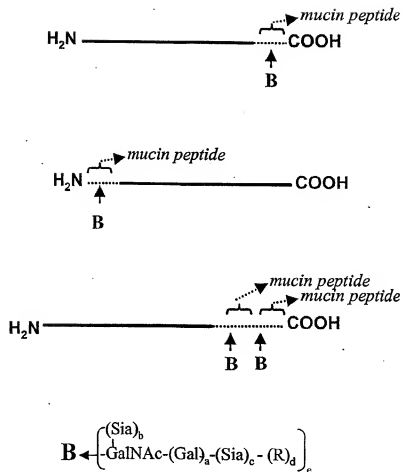
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 52D

238/498



a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 52E

239/498

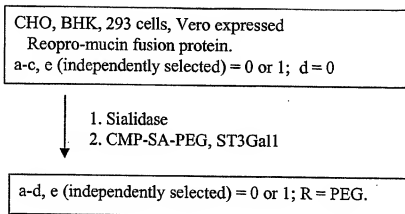


FIG. 52F

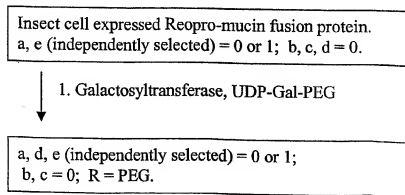


FIG. 52G

240/498

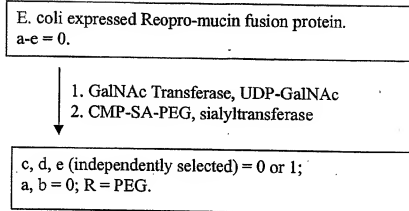


FIG. 52H

242/498

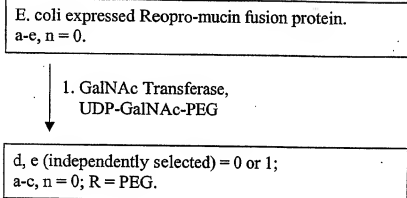


FIG. 52J

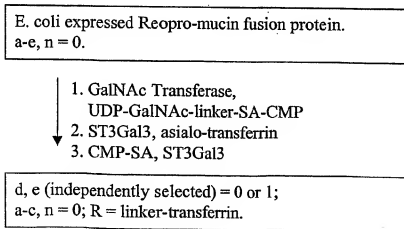


FIG. 52K

243/498

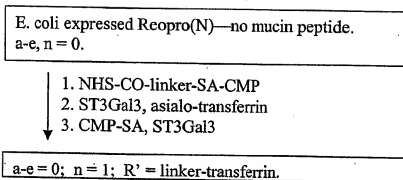
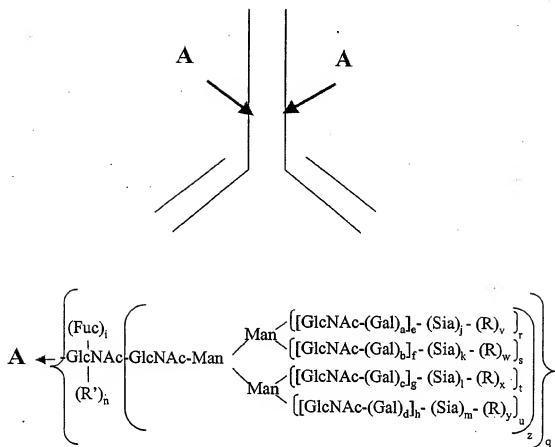


FIG. 52L

244/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 53A

245/498

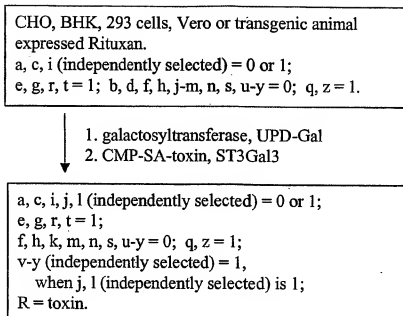


FIG. 53B

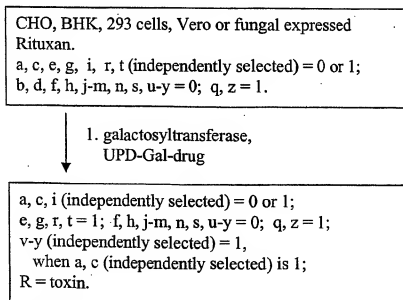


FIG. 53C

246/498

Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

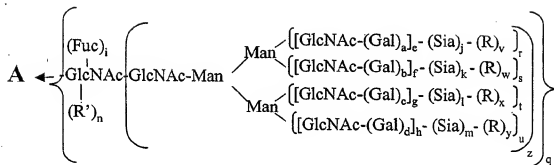
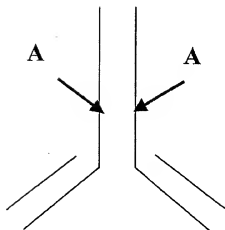
↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 53D

247/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 53E

248/498

CHO, BHK, 293 cells, Vero or transgenic animal
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when j, l (independently selected) is 1;
R = PEG.

FIG. 53F

Fungi, yeast or CHO expressed Rituxan.

e, g, i, r, t, v, x (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u, w, y = 0; q, z = 1;

R (independently selected) = mannose, oligomannose,
polymannose.

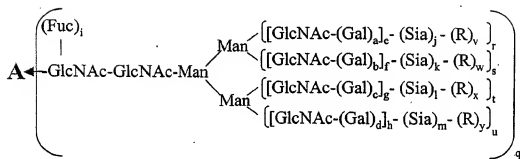
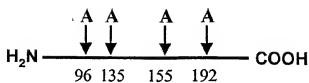


1. mannosidases (alpha and beta)
2. GNT-I,II, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal-radioisotope

a-m, r-z = 0; q, n = 1;
R' = -Gal-radioisotope complex.

FIG. 53G

249/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = mannose, polymer.

FIG. 54A

250/498

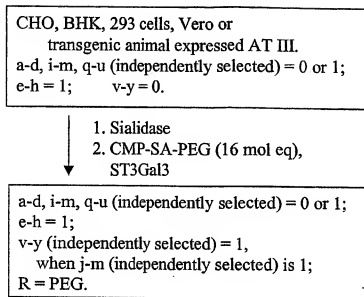


FIG. 54B

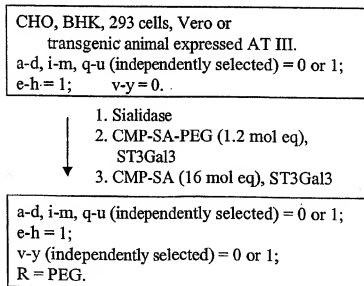


FIG. 54C

251/498

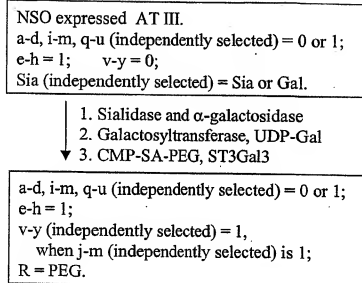


FIG. 54D

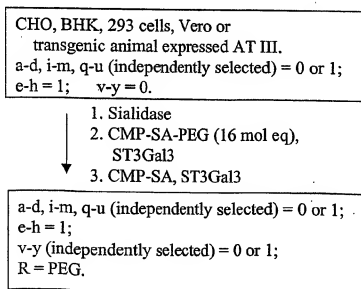


FIG. 54E

252/498

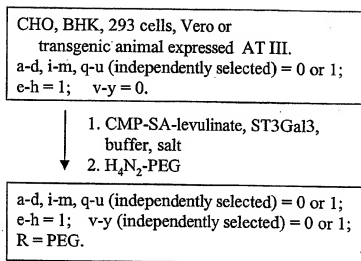


FIG. 54F

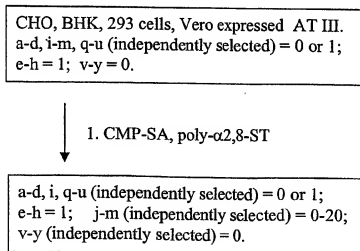
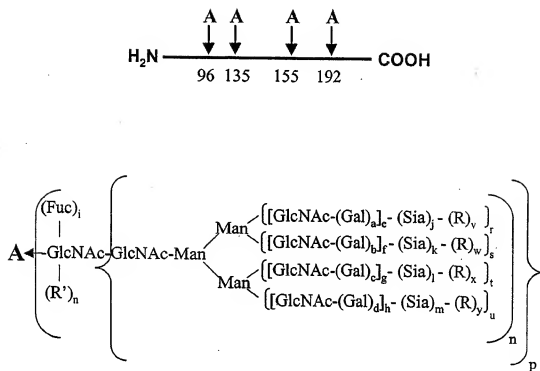


FIG. 54G

253/498



a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100.

R = polymer, linker, mannose.

R' = H, sugar, glycoconjugate.

FIG. 54H

254/498

Insect, yeast or fungi cell expressed AT III.
 a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, q, r, t (independently selected) = 0 or 1;
 p = 1.

↓
 1. GNT 1, UDP-GlcNAc-PEG

a, i, q, r, -u (independently selected) = 0 or 1;
 b-g, j-n, s-u, w-y = 0; p = 1;
 v (independently selected) = 1,
 when a (independently selected) is 1;
 R = PEG.

FIG. 54I

Yeast expressed AT III.
 a-n = 0; q-y (independently selected) = 0 to 1;
 p = 1;
 R (branched or linear) = Man, oligomannose.

↓
 1. Endoglycanase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0;
 n (independently selected) = 0 or 1;
 R' = -Gal-Sia-PEG.

FIG. 54J

255/498

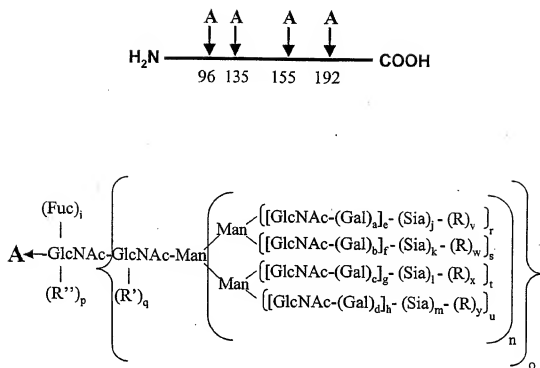
CHO, BHK, 293 cells, Vero expressed AT III.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin
treated with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 54K

256/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer.

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 54L

257/498

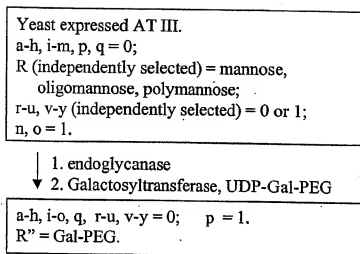


FIG. 54M

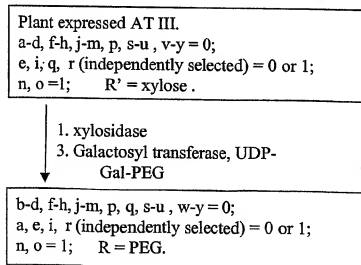


FIG. 54N

258/498

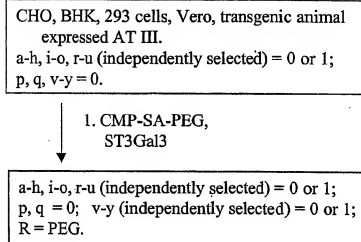
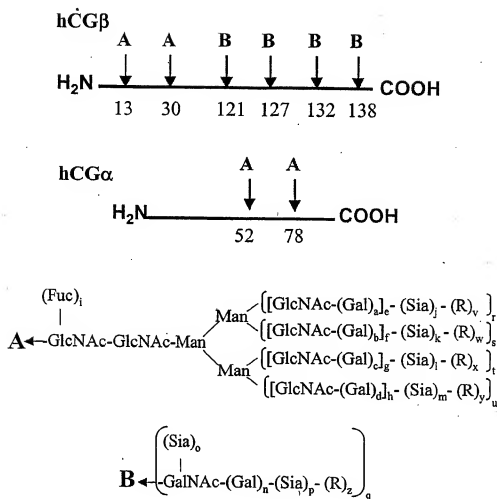


FIG. 54O

259/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer

FIG. 55A

260/498

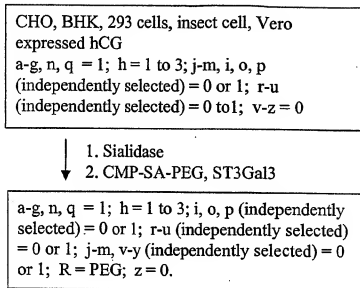


FIG. 55B

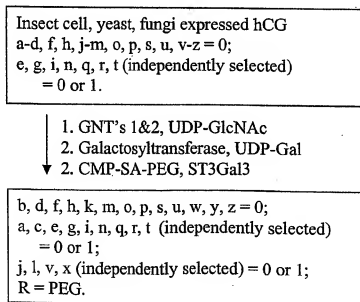


FIG. 55C

261/498

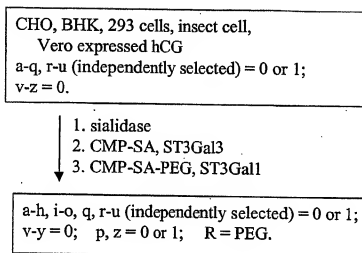


FIG. 55D

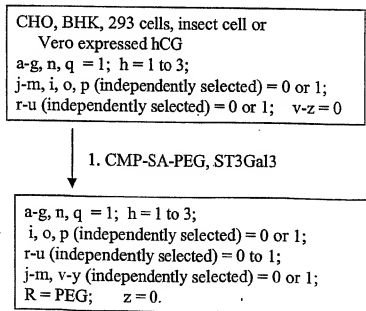


FIG. 55E

262/498

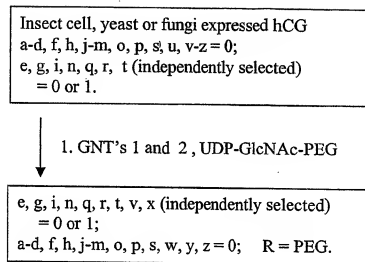


FIG. 55F

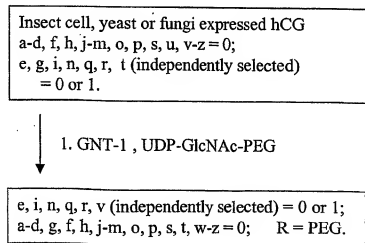


FIG. 55G

263/498

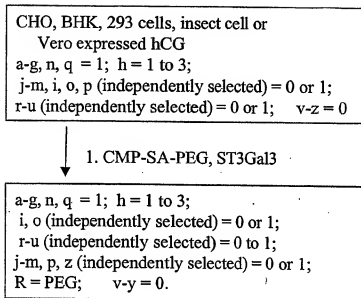


FIG. 55H

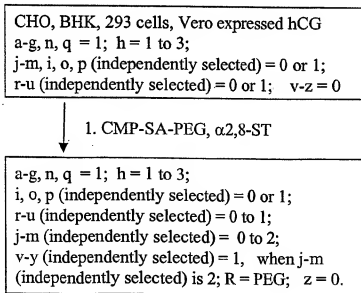


FIG. 55I

264/498

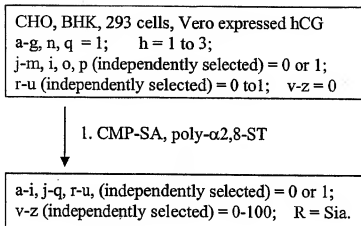
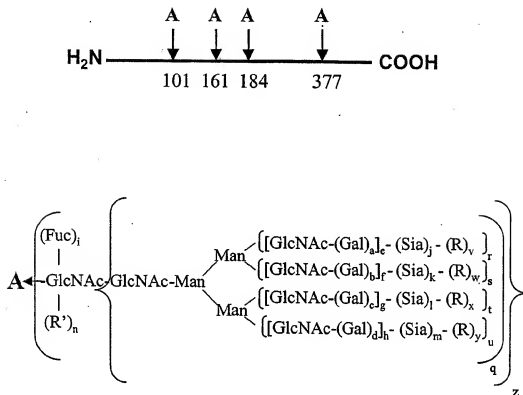


FIG. 55J

265/498



a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 56A

266/498

CHO, BHK, 293 cells, insect cells, Vero expressed and secreted alpha-galactosidase
 a-h, i-m, q-u (independently selected) = 0 or 1;
 z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

- ↓
 1. Endo-H
 2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1; and when z = 0 and q = 1,
 then n (independently selected) = 0 or 1;
 R' = Gal-PEG-transferrin.

FIG. 56B

CHO, BHK, 293 cells, Insect cells,
 Vero expressed and secreted alpha-galactosidase
 a-h, i-m, q-u (independently selected) = 0 or 1; z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

- ↓
 1. Sialidase
 2. CMP-SA-linker-Mannose-6-phosphate
 ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1;
 n = 0; z = 1; R = mannose-6-phosphate; and when a-n = 0, then r-u (independently selected) = 0 or 1;
 v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

FIG. 56C

267/498

NSO expressed alpha-galactosidase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;
v-y (independently selected) = 1, when j-m (independently selected) is 1; R = mannose-6 phosphate

FIG. 56D

CHO, BHK, 293 cells, Insect cells, Vero expressed and secreted alpha-galactosidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;

n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;

R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
 2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0; z = 1; R = PEG; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y = 0-100; R = mannose or mannose with mannose-6-phosphate.

FIG. 56E

268/498

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate;
v-y (independently selected) = 0 or 1;
R = mannose-linker-ApoE.

FIG. 56F

CHO, BHK, 293 cells, Insect cells, Vero, yeast,
fungi expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H
2. galactosyltransferase,
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;
R' = galactose-linker-alpha2-macroglobulin.

FIG. 56G

269/498

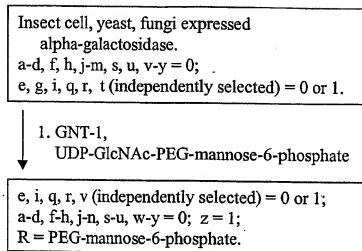


FIG. 56H

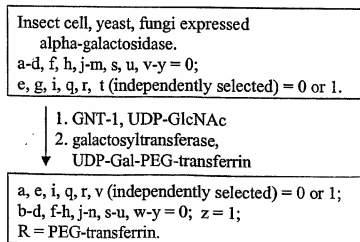


FIG. 56I

270/498

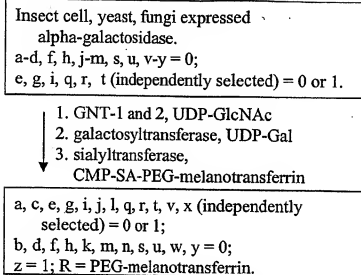
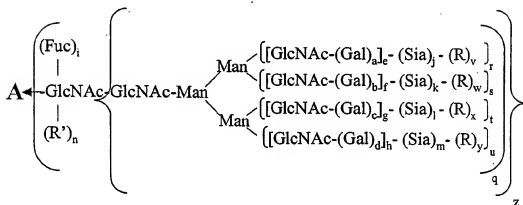
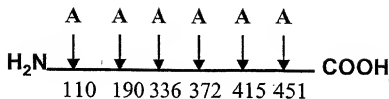


FIG. 56J

271/498



a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 57A

272/498

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Endo-H
↓
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1; and when z = 0 and q = 1, then n
(independently selected) = 0 or 1; R' = Gal-PEG-transferrin.

FIG. 57B

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
↓
2. CMP-SA-linker-Mannose-6-phosphate ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;
z = 1; R = mannose-6-phosphate; and when a-n = 0,
then r-u (independently selected) = 0 or 1;
v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 57C

273/498

NSO expressed alpha-iduronidase.

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;

v-y = 0; Sia (independently selected) = Sia or Gal.

↓ 1. Sialidase and α -galactosidase

2. Galactosyltransferase, UDP-Gal

↓ 3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = mannose-6 phosphate

FIG. 57D

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;

n, v-y = 0; and when a-n = 0, then r-u (independently

selected) = 0 or 1; v-y (independently selected) = 0-100;

R = mannose or mannose with mannose-6-phosphate.

↓ 1. Sialidase

2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;

z = 1; R = PEG; and when a-n = 0, then r-u

(independently selected) = 0 or 1; v-y = 0-100;

R = mannose or mannose with mannose-6-phosphate.

FIG. 57E

274/498

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-iduronidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1; j-m (independently
selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate;
v-y (independently selected) = 0 or 1;
R = mannose-linker-ApoE.

FIG. 57F

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-iduronidase.
a-i, v-y = 0; q (independently selected) = 0 or 1;
z = 1; r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H
2. galactosyltransferase,
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;
R' = galactose-linker-alpha2-macroglobulin.

FIG. 57G

275/498

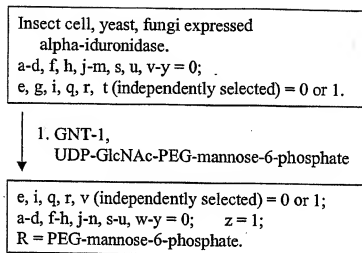


FIG. 57H

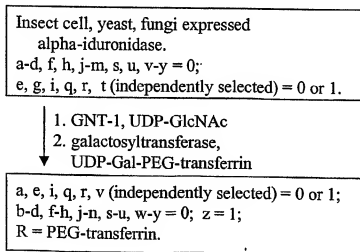


FIG. 57I

276/498

Insect cell, yeast, fungi expressed
alpha-iduronidase.

a-d, f, h, j-m, s, u, v-y = 0;

c, g, i, q, r, t (independently selected) = 0 or 1.

- ↓ 1. GNT-1 and 2, UDP-GlcNAc
2. galactosyltransferase, UDP-Gal
3. sialyltransferase,
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x

(independently selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0; z = 1;

R = PEG-melanotransferrin.

FIG. 57J

277/498

FIG. 58A

ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT
GCTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCCTTGAGCAGCTG
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA
GCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT
CCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCCTCTGCT
TTCCAGCGCCGGGCAGGAGGGGTCCTGGTTGCCTCCCATCTGCAGAG
CTTCTGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCCAGCCCTG
A

FIG. 58B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
Leu Ala Gln Pro

278/498

FIG. 59A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA
AGAAATATAGTTATCAAGTTAAGTAAAATGTCAATAGCCTTTTAATTTA
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAACATTAACTTTAT
ACTTTTAAATTATATAGAAATAGAGATATACATAGGATATGTAAA
TAGATACACAGTGTATATGTGATTAAAAATATAATGGGAGATTCAATC
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA
AAGAGTGATAAAGAAAGCAAAAAGAGAAGTAGAAAAGTAACACAGG
GGCATTGTGGAAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCTGGGTAGCAGG
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTTTTCTCC
TGCTTGAAGGACAGACATGACTTTGGATTTCAGGAGGAGTTTGG
CAACCAGTTCCAAAAGGCTGAAACCATCCCTGTCTCCATGAGATGA
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT
GGGATGAGACCCTCCTAGACAAAATTCTACACTGAACTCTACCAGCAG
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT
TCCAAAGAATCACTCTCTATCTGAAAAGAGAAGAAATACAGCCCTTGT
GCCTGGGAGGTTGTGAGAGCAGAAATCATGAGATCTTTTTCTTTGTCA
ACAAACTGTGAAGAAAGTTTAAGAAGTAAGGAATGAAAACCTGGTTCA
ACATGGAAATGATTTTCATTGATTCGTATGCCAGCTACCTTTTTATG
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACTATTGTATTCAG
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT
ATCTATTTAAATATTTTTAAAAATATTATTTATTTAACTATTTATAAAAC
AACTTATTTTGTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTTGTGTTGTT
CATTGAACCTTTTGTATGGAACCTTTGTACTTGTATTCTCTTAAAAATG
AAATCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA
CTTCATTTGTCCATCAATATTATATTCAAGATATAAGTAAAAATAAAC
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC
TAACAAATACAATTCTGCTCTCTCTGTGTATTTGATTTTGTATGAAAA
AAACTAAAAATGGTAATCATACTTAATTATCAGTTATGGTAAATGGT
ATGAAGAGAAGAAGGAACG

279/498

FIG. 59B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser
 Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr
 Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
 Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
 Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu
 Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
 Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
 Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
 Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu
 Arg Ser Lys Glu

FIG. 59C

ATGGCCCTCCTGTTCCCTCTACTGGCAGCCCTAGTGATGACCAGCTAT
 AGCCCTGTTGGATCTCTGGGCTGTGATCTGCCTCAGAACCATGGCCTA
 CTTAGCAGGAACACCTTGTTGCTTCTGCACCAAATGAGGAGAATCTCC
 CCTTTCTGTGTCTCAAGGACAGAAGAGACTTCAGGTTCCCCAGGAG
 ATGGTAAAAGGGAGCCAGTTGCAGAAGGCCCATGTTCATGTCTGTCT
 CCATGAGATGCTGCAGCAGATCTTCAGCCTCTTCCACACAGAGCGCTC
 CTCTGCTGCCTGGAACATGACCCTCCTAGACCAACTCCACACTGGACT
 TCATCAGCAACTGCAACACCTGGAGACCTGCTTGCTGCAGGTAGTGG
 GAGAAGGAGAAATCTGCTGGGGCAATTAGCAGCCCTGCACCTGACCTTG
 AGGAGGTACTTCCAGGGAATCCGTGTCTACCTGAAAGAGAAGAAATA
 CAGCGACTGTGCCTGGGAAGTTGTCTCAGAATGGAAATCATGAAATCCT
 TGTTCCTTATCAACAAACATGCAAGAAAGACTGAGAAGTAAAGATAGA
 GACCTGGGCTCATCTTGA

FIG. 59D

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr Ser Pro Val
 Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr
 Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu Lys Asp
 Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser Gln Leu Gln Lys
 Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His
 Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr
 Gly Leu His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
 Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe
 Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Val
 Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met Gln Glu Arg
 Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser

280/498

FIG. 60A

ATGACCAACAAGTGTCTCTCTCCAAATTGCTCTCCTGTTGTGCTTCTCC
 ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTACAAAGA
 AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG
 GCTTGAATATTGCCTCAAGGACAGGATGAACCTTGACATCCCTGAGG
 AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGATTGACC
 ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA
 TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA
 TGTCTATCATCAGATAAACCATCTGAAGACAGTCTTGAAGAAAAAC
 TGGAGAAAGAAGATTTTACCAGGGGAAAACATGAGCAGTCTGCAC
 CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA
 GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA
 ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT
 CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTCAAGCATTCTTC
 AACCAGCAGATGCTGTTTAAGTGACTGATGGCTAATGTACTGCAAAAT
 GAAAGGACACTAGAAGATTTTGAAATTTTATTAAATTATGAGTTATT
 TTTATTTAT TTAATTTTATTTTGGAAAAATAAATTATTTTGGTGC

FIG. 60B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala
 Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
 Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp
 Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu
 Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
 Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp
 Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile
 Leu His Tyr Leu Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
 Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

281/498

FIG. 61A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT
CCTGCACCGGCGCCGGCGCGCCAACGCGTTCTTGAGGAGCTGCGGG
CGGGCTCCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA
GAATGGGGGCTCCTGCAAGGACCAGTCCAGTCCATATATCTGCTTCT
GCCTCCCCTGCCTTCGAGGGCCGGAACCTGTGAGACGCACAAGGATGAC
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG
TGACCACACGGGCACCAAGCGCTCCTGTGCGGTGCCACGAGGGGTACT
CTCTGCTGGCAGACGGGGTGTCTGCACACCCACAGTTGAATATCCA
TGTGGA AAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAAACCCCA
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCAAAGGGGAGTGTCCA
TGGCAGGTCTCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACCAACACGACATC
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTGGTG
CCCCTCTGCCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC
GTGCTCTTCTCATTTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGG
CGCCACGGCCCTGGAGCTCATGGTGTCTCAACGTGCCCGGCTGATGA
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT
ATCAGGAGTACATGTTCTGTGCCGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGGCCACATGCCACCCACTACCGGG
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA
ACCGTGGGGCACTTTGGGGTGTAACCAGGGTCTCCAGTACATCGA
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCAGGAGTCTCTCC
TGCGAGCCCCATTTC

282/498

FIG. 61B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

283/498

FIG. 62A

ATGCAGCGCGTGAACATGATCATGCGCAGAATCACCAAGCCTCATCAC
CATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTT
GATCATGAAAAACGCCAACAAAAATCTGAATCGGCCAAAAGAGGTATAA
TTCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAAT
GTATGGAAGAAAAGTGTAGTTTTGAAGAACCACGAGAAGTTTTTGAA
AACACTGAAAAGACAACCTGAATTTTGGAAGCAGTATGTTGATGGAGA
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG
ACATTAATTCCATGAATGTTGGTGTCCCTTTGGATTGGAAGGAAAGA
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT
GAGGGATATCGACTTGCAGAAAAACCAGAAGTCCTGTGAACCAGCAGT
GCCATTTCCATGTGGAAGAGTTTCTGTTTCAAAACTTCTAAGCTCAC
CCGTGCTGAGGCTGTTTTTCTGATGTGGACTATGTAATCCTACTGA
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA
GGCTCTATCGTTAATGAAAAATGGATTGTAACCTGCTGCCACTGTGTT
GAAACTGGTGTTAAAAATTACAGTTGTCGCAGGTGAACATAATATTGA
GGAGACAGAAACATACAGAGCAAAAAGCGAAATGTGATTGAGCAATT
ATTCTCACCACAACATAAATGCAGCTATTAATAAGTACAACCATGA
CATTGCCCTTCTGGAACCTGGACGAACCCCTAGTGTCAAAACAGCTACG
TTACACCTATTTCATTGCTGACAAGGAATACACGAACATCTTCTCA
AATTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTGAC
CGAGCCACATGCTTCGATCTACAAAAGTTACCATCTATAACAACAT
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTGATGTCAGGAG
ATAGTGGGGGACCCCATGTTACTGAAGTGGAAGGGACCAAGTTCTTA
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAAATA
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAAGGAAA
AAACAAAGCTCACITTAATGAAAGATGGATTTC AAGGTTAATTCATT
GGAATTGAAAATTAACAG

284/498

FIG. 62B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu
 Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala
 Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe
 Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu
 Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr
 Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys
 Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn
 Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys
 Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu
 Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser
 Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr
 Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser
 Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
 Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val
 Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr
 Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn
 Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn
 His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr
 Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
 Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln
 Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe
 Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser
 Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu
 Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr
 Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

285/498

FIG. 63A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCA
GAATGCACGCTACAGGAAAACCCATTCTTCTCCAGCCGGGTGCCCC
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCC
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTACCTCAG
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG
GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT
GTGAGATAAACTCTCCTTTTCCTTACCATACCACTTTGACACGCTTC
AAGGATATACTGCAGCTTTACTGCCTTCCCTCCTTATCCTACAGTACAA
TCAGCAGTCTAGTCTTTTCATTTGGAATGAATACAGCATTAAGCTTG
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 63B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

286/498

FIG. 63C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCCC
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG
ATTGTA CTGTGCGAGGCCTGGGGCCAGCTACTGCTCCTTTGGTGAAA
TGAAAGAATAA

FIG. 63D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

287/498

FIG. 64A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT
GCACCGCCGAGCTTCCCCGGATGAGGGCCCCCGGTGTGGTCACCCGG
CGCGCCCCAGGTGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG
GTGCACGAATGTCCTGCTGGCTGTGGCTTCTCCTGTCCCTGCTGTG
CTCCTCTGGGCTCCCAGTCTGGGCGCCCCACCACGCCTCATCTGT
GACAGCCGAGTCTTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAAGGAT
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG
CTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGCGAGCCCAAGAAG
AAGCCATCTCCCCCTCAGATGCGGCCTCAGCTGCTCCACTCCGAACA
ATCACTGCTGACACTTTCGCAAACTCTTCCGAGTCTACTCCAATTC
CTCCGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC
TCACCAACATTGCTGTGTCCACACCCCTCCCCCGCCACTCCTGAACCCC
GTGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC
AACTCTGAGATCTAAGGATGTACAGGGCCAACTTGAGGGCCAGAG
CAGGAAGCATTAGAGAGCAGCTTTAAACTCAGGGACAGGCCATG
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC
AGGACACGCTTTGGAGGCGATTTACCTGTTTTCGCACCTACCATCAGG
GACAGGATGACCTGGGAACTTAGGTGGCAAGCTGTGACTTCTCCAG
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCCTCTGG
CTCTCATGGGGTCCAAGTTTGTGTATTCTTCAACCTCATTGACAAGA
ACTGAAACCACCAAAAAAAAAAAAAA

288/498

FIG. 64B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu Leu Ser
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

FIG. 65

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

289/498

FIG. 66A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT
CTCTGCACCCGCCCCGCTCGCCAGCCCCAGCACGCAGCCCTGGGAGC
ATGTGAATGCCATCCAGGAGGCCGGCGTCTCCTGAACCTGAGTAGA
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAAT
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA
ACCTGAAGGACTTTCTGCTTGTATCCCCTTTGACTGCTGGGAGCCAG
TCCAGGAGTGA

FIG. 66B

Met Trp Leu Gln Ser Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

290/498

FIG. 67A

ATGAAATATACAAGTTATATCTTGCTTTTCAGCTCTGCATCGTTTGG
GGTTCTCTTGCTGTTACTGCCAGGACCCATATGTAAAAAGAAGCAGA
AAACCTTAAGAAATATTTTAATGCAGGTCATTTCAGATGTAGCGGATA
ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACT
TTTTAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT
GAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTG
AACTGTGCGCCAGCAGCTAAAAACAGGGAAGCGAAAAAGGAGTCAGAT
GCTGTTTCGAGGTGCAAGAGCATCCCAAGTAA

FIG. 67B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
Leu Lys Asn Trp Lys Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

291/498

FIG. 68A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC
CAGGAACCTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT
GACCACCGGAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAAGCCTTC
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG
ATTACGTGGAGAAGGGTACTCAAGGGAATTTGTGGATTTGGTCAAG
GAGCTTGACAGAGACACAGTTTTTGTCTCTGGTGAATTACATCTTCTTT
AAAGGCAAAATGGGAGAGACCCCTTTGAAGTCAAGGACACCGAGGAAG
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG
AAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTCCAG
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC
CACGATATCATCACCAAGTTTCTGGAAAATGAAGACAGAAGGTCTGC
CAGCTTACATTACCCAACTGTCCATTACTGGAACCTATGATCTGAA
GAGCGTCTGGGTCAACTGGGCATCACTAAGGTCTTTCAGCAATGGGG
CTGACCTCTCCGGGGTACAGAGGAGGCACCCCTGAAGCTCTCCAAG
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAAGGACTGAAGC
TGCTGGGGCCATGTTTTAGAGGCCATACCCATGTCTATCCCCCGGA
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAAATAC
CAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT
AACTGCCTCTCGTCTCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC
CTGGATGACATTAAAGAAGGGTTGAGCTGG

292/498

FIG. 68B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val
Phe Ala LeuVal Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys
Phe Leu Glu Asn Glu AspArg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val
Val Asn Pro Thr Gln Lys

293/498

FIG. 69A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTT
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGGGTCT
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTCAAGTCCTTCCA
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCTGGGCATCAGGT
GCCCCCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCGACCTTTCCT
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG
GCCTGCTACTGACCCTGCAGCCAGAACAGAAGTCCAGAAAAGTGAAG
GGATTGGAGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC
CTGTACACCCCTGCCCAAAATTTGCTACTTAAATCGTACTTCTCTGAA
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCGA
GTTGCACAACCTCAGCCTCCCAGAGGAAGATACCAAGCTCAAGATAC
CCCTGATTACCCGAGCCCTGCAGTTGGCCAGCGTCCGTTTCACTCC
TTGCCAGCCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG
GTGAATGGGAAGGGGTCACTCAAGGACAGCCCGGAGACATCTACC
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG
AGCACAAGTATACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTACCCCT
GAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCTACCCCTCGCC
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACGC
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACTGGACTTTCT
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA
ACACCATGCTCTTTGCCTCAGAGGCCCTGTGTGGGCTCCAAGTCTGGG
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC
CACAGCATCATCAGAACCTCCTGTACCATGTGTGCGGTGGACCGAG
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA
CTTGTGCGACAGTCCCATCATTGTAGACATCACCAGGACACGTTTAA
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC
TGAGGGCTCCCAAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC
TGGACGCAGTGGCAGTGTGATGCATCCCGATGGCTGTCTGTTGTGGTCTG
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG
CTGTGGGCTTCTCGAGACAATCTCACCTGGCTACTCCATTACACCT
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCAGTGG
GCTCAGCCTGGGCTATTAAAGGGACAGAGTCAGTCAACGCTGTCTG
TGACTAAAGAGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

294/498

FIG. 69A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCTCTAGGTGGT
 GCCCAGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTCT
 CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT
 TGGAAACT

FIG. 69B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser
 Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser
 Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys
 Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr
 Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly
 Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 Lys Phe Gln Lys Val Lys Gly Phe Gly Ala Met Thr Asp Ala Ala Ala Leu
 Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser
 Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
 Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser
 Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu
 Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
 Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile
 Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu
 His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
 Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp
 Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg
 Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val
 Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
 Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro
 Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser
 Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu
 Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr
 Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu
 Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn
 Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
 Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

295/498

FIG. 70A

ATGGATGCAATGAAGAGAGGGGCTCTGCTGTGTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCCGATTACAGAA
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAACGCA
GATGATATACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA
GCAACCGGGTGGAATATTGCTGGTGCAACAGTGGCAGGGCAGAGTGC
CACTCAGTGCCTGTCAAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG
GGGCACCTGCCAGCAGGGCCCTGTACTTCTCAGATTTCGTGTGCCAGTG
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCA
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGGCACGTGGAGCAC
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG
GCCTGGGGAACCAACTACTGCAGAAACCCAGATCGAGACTCAAA
GCCCTGGTGCTACGTCTTTAAGCGGGGAAGTACAGCTCAGAGTTCT
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC
CTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACAC
AGCACAGAACCCCAAGTGGCCAGGCACTGGGCCCTGGGCAAAACATAATT
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG
GAGGGCTCTTTCGCCGACATCGCCTCCACCCCTGGCAGGCTGCCATCT
TTGCCAAGCAGCAGGAGGTGCGCCGGGAGAGCGGTTCTGTGCGGGGGC
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
TACATTGTCCATAAGGAATTTCGATGACACTTACGACAATGACAT
TGCGCTGCTGCAGCTGAAATCGGATTTCGTCCCGCTGTGCCCAGGAGA
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG
CCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC
CTTGCTCTCTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTACAGCT
GTACCCATCCAGCCGCTGCACATCACAAACATTTACTTAACAGAAAC
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGGCCC
CAGGCAAACTTGACGACGCCTGCCAGGGCGATTCCGGGAGGCCCCCT
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT
GGGGCCTTGGGCTGTGGACAGAAGGATGTCCGGGTGTGTACACCAAG
GTTACCAACTACCTAGACTGGATTTCGTGACAACATGCGACCGTGACC
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

296/498

FIG. 70B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys
Thr Asn Trp Asn Ser Ser-Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Gln Lys Phe Glu Val Glu Lys
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg
Asp Asn Met Arg Pro

297/498

FIG. 71A

ATCACTCTCTTAACTCACTACTCACATTAACCTCAACTCCTGCCACAA
TGTAACAGGATGCAACTCCTGTCTTGCAATTGCACTAATTCTTGCACTTG
TCACAAACAGTGCACCTACTTCAAGTTCGACAAAGAAAACAAAGAAA
ACACAGCTACAACCTGGAGCATTACTGCTGGATTTACAGATGATTTTG
AATGGAATTAATAATTACAAGAATCCCCAAACTCACCAGGATGCTCAC
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC
AGTGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA
GCTCAAAGCAAAAACTTTCACTTAAGACCCAGGGACTTAATCAGCAA
TATCAACGTAATAGTTCTGGAACATAAGGGATCTGAAACAACATTCA
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAAGTTGATAA
TTAAGTGCTTCCCACTTAAACATATCAGGCCTTCTATTTATTTATTTA
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG
TAACTATTATTCTTAATCTTAAAACTATAAATATGGATCTTTTATGAT
TCTTTTTGTAAAGCCCTAGGGGCTCTAAAATGGTTTACCTTATTTATCC
CAAAAAATATTTATTTATGTTGAATGTTAAATATAGTATCTATGTAG
ATTGGTTAGTAAACTATTTAATAAAATTTGATAAATATAAAAAAAAAA
AAACAAAAAAAAAAAA

FIG. 71B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
Gln Ser Ile Ile Ser Thr Leu Thr

298/498

FIG. 72A-1

ATGCAAAATAGAGCTCTCCACCTGCTCTTTCTGTGCCTTTTGCATTCT
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGTCA
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG
ATTTCTCCTAGAGTGC AAAATCTTTCCATTCAACACCTCAGTCGT
GTCAAAAAGACTCTGTTGTAGAATTCACGGATCACCTTTTCAACAT
CGCTAAGCCAAAGGCCACCTGGATGGGTCTGCTAGGCTCTACCATCC
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT
TCCCATCCTGTGAGTCTTCATGCTGTTGGTGTATCCTACTGGAAGCT
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG
AAGATGATAAAGTCTTCCCTGGTGAAGCCATACATATGTCTGGCAG
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG
CCTCATTTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG
AAAAGACACAGACCTTGCACAAAATTTATACTACTTTTGTCTGTATTTG
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATCA
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACCTCTGAA
GTGCACTCAATATTCTCGAAGGTACACATTTCTGTGAGGAACCAT
CGCCAGGCGTCTTGGAAAATCTCGCCAATAACTTTCTTACTGCTCAA
ACACTCTTGATGGACCTTGGACAGTTCTACTGTTTGTGCATATCTCTT
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT
CCAGGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG
ACTATGATGATGATCTTACTGATTCTGAAATGGATGCTGGTCAAGTTTG
ATGATGACAACCTCTCCTTCTTATCCAAATTCGCTCAGTTGCCAAGA
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC
TGGGACTATGCTCCCTTAGTCTCGCCCCGATGACAGAAGTTATAAA
AGTCAATATTTGAACAAATGGCCCTCAGCGGATTGGTAGGAAGTACAA
AAAAGTCCGATTTATGGCATAACAGATGAAACCTTTAAGACTCGTG
AAGCTATTTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG
AAGTTGGAGACACACTGTTGATTATTTAAGAATCAAGCAAGCAGA
CCATATAACATCTACCCTCACGGAATCACTGATTCGCTCTTTGTAT
TCAAGGAGATTACCAAAAGGTGTAAAAACATTTGAAGGATTTTCCAAT
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGAAGTGTAGAAG
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC
TCCTCATCTGTACAAAAGAATCTGTAGATCAAAGAGGAAACCGATA
ATGTCAGACAAGAGGAATGTCATCCTGTTTCTGTATTTGATGAGAAC
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTCTCCCCAATCCA
GCTGGAGTGCAGTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT
GCACAGATCAAGTGGCTATGTTTTGATAGTTTGAGTTGTCAAGTTTG
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTTGGAGACAGAG
CTGACTTCCTTTCTGTCTCTTCTCTGGATATACCTTCAAACACAAAAT

299/498

FIG. 72A-2

GGTCTATGAAGACACACTCACCTATTCCCATTCTCAGGAGAAACTGT
CTTCATGTGCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA
ACTCAGACTTTCCGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT
AGTTGTGACAAGAACACTGGTGATTATTACGAGGACAGTTATGAAGA
TATTTTCAGCATACTTGTCTGAGTAAAAACAATGCCATTGAACCAAGAA
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCCAAAAGCAATTT
AATGCCACCACAATTCCAGAAAAATGACATAGAGAAGACTGACCCCTG
GTTTGACACAGAACACCTATGCCTAAAAATACAAAATGTCTCCTCTA
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT
CCTTATCTGTGATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA
CACTTCAGGCCACAGCTCCATCAGTGGGGACATGGTATTTACCCC
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAACTGGGGACAACTG
CAGCAACAGAGTTGAAGAAACTTGATTTCAAAGTTTCTAGTACATCA
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT
GATAATACAAGTTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT
AGTCAATTAGATACCACTCTATTTTGGCAAAAAGTCATCTCCCCTTACT
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAAATGATTCAAA
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA
AAAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGAAAAAGA
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAAGTT
AGCATCTCTTTGTTAAAGACAAACAAAACCTTCCAATAATTCAGCAACT
AATAGAAAGACTCAGCATTGATGGCCCATCTATTATAATGAGAATAG
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAA
AAGTGACACCTTTGATTTCATGACAGAATGCTTATGGACAAAAATGCT
ACAGCTTTGAGGCTAAATCATATGTCAAATAAAACTACTTCATCAAAA
AAACATGGAAATGGTCCAACAGAAAAAGAGGGCCCCATCCACCA
GATGCACAAAATCCAGATATGTCGTTCTTTAAGATGCTATTCTTGCCA
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG
AAAAATCTGTGGAAGGTCAGAATTTCTGTCTGAGAAAAACAAAGTG
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA
TGTTTTTTCCAAGCAGCAGAAACCTATTCTTACTAAGTTGGATAATT
TACATGAAAAATAATACACACAATCAAGAAAAAAAATTCAGGAAGA
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC
AGATACATACAGTGACTGGCAGTAAAGAAATTCATGAAGAACCTTTTC
TTACTGAGCACTAGGCAAAATGTAGAAGGTTTCATATGACGGGGCATA
TGCTCCAGTACTTCAAGATTTTAGGTCATTAATGATTCAACAAATAG
AACAAAGAAACACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA
AACTTGGAAAGGCTTGGGAAATCAAACAGCAAATGTAGAGAAATAT
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAAATTTG
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCACTA

FIG. 72A-3

300/498

GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCCCTCACAC
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAAATAGA
TCTCCATTACCCATTGCAAAGGTATCATTTCCATCTATTAGACCTA
TATATCTGACCAGGGTCTATTCCAAGACAACCTTCTCATCTTCCAG
CAGCATCTTATAGAAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT
TTCTTACAAGGAGCCAAAAAAATAACCTTTCTTTAGCCATTCTAACC
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC
GAAACCAGACTTGCCCCAAACATCTGGCAAAGTTGAATTGCTTCCAA
AAGTTCACATTTATCAGAAGGACCTATTCCTACGGAAACTAGCAATG
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA
CAGAGGGAGCGATTAAGTGAATGAAGCAAACAGCCTGGAAAAAGT
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAGAGACTCCCTCAA
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC
AAAAGAAGAGTGGAAAATCCCAAGAGAAAGTCAACCAGAAAAAACAGCT
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAAGCAAT
CATGCAATAGCAGCAATAAAATGAGGGACAAAAATAAGCCGAAATAG
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA
AACCCACCAGTCTTGAAACGCCATCAACGGGAAAATAACTCGTACTAC
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAAAT
AGAGCCCCCGCAGCTTTCAAAAAGAAACACGACACTATTTTATTGCTG
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAGAAAGT
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT
GGAGAACTCAAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC
AGAAGTTGAAGATAATATCATGGTAACTTTCAGAAATCAGGCCTCTC
GTCCCTATTCTTCTATTCTAGCCTTATTCTTATGAGGAAGATCAGAG
GCAAGGAGCAGAACCTAGAAAAAATTTGTCAAGCCTAATGAAACCA
AAACTTACTTTTGAAAAGTGCAACATCATATGGCAACCCACTAAAGAT
GAGTTTGACTGCAAAGCCTGGGCTTATTCTCTGATGTTGACCTGGAA
AAAGATGTGCACTCAGGCCTGATTGGACCCCTTCTGGTCTGCCACACT
AACACACTGAACCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT
TGCTCTGTTTTTACCATCTTTGATGAGACCAAAAGCTGGTACTTCACT
GAAAAATATGGAAGAAACTGCAGGGCTCCCTGCAATATCCAGATGGA
AGATCCCACTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAAACATCCATTCT
ATTCAATTCAGTTGGACATGTGTTCACTGTACGAAAAAAAGAGGAGTA
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGGAGACAGTGA

FIG. 72A-4

301/498

AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGGAATGCCTTATTGG
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA
TAAGTGTGAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG
CCAGACTTCATTATTCCGGATCAATCAATGCTGGAGACCAAGGAG
CCCTTTTTCTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTAC
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA
CTTATCGAGGAAATCCACTGGAACCTTAATGGTCTTCTTTGGCAATG
TGGATTCATCTGGGATAAAAAACAATATTTTTAACCCCTCCAATTATTG
CTCGATACATCCGTTTGCACCCAACCTCATTATAGCATTTCGAGCACTC
TTCGCATGGAGTTGATGGGCTGTGATTAAATAGTTGCAGCATGCCAT
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA
TCCACTTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA
CAGGAGTAACTACTCAGGGAGTAAAATCTCTGCTTACCAGCATGTAT
GTGAAGGAGTTCCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC
TCTCTTTTTTTCAGAAATGGCAAAGTAAAGGTTTTTTCAGGAAATCAAGA
CTCCTTCACACCTGTGGTGAACCTCTCTAGACCCACCCTTACTGACTCG
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC
CACTGCAGCACCTGCCACTGCCGTCACCTCTCCCTCCTCAGTCCAGG
GCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGC
AGACACTGCCTTGAAAGCCTCCTGAATTAACATATCATCAGTCTGCATT
TCTTTGGTGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACTCTTA
CCTATTTTCTGCAGCTGTCTCCAGATTACTCTTCTTCCAATATAACT
AGGCAAAAAGAAGTGAGGAGAAAACCTGCATGAAAGCATTCTTCCCTG
AAAAGTTAGGCCTCTCAGAGTCACCACTTCTCTGTGTAGAAAACT
ATGTGATGAACTTTGAAAAAGATATTTATGATGTTAACATTCAGGT
TAAGCCTCATACGTTTAAAAATAAACTCTCAGTTGTTTATTATCCTGA
TCAAGCATGGAACAAGAAGCATGTTTCAGGATCAGATCAATACAATCTT
GGAGTCAAAAAGGCAAAATCATTTGGACAATCTGCAAAATGGAGAGAA
TACAATAACTACTACAGTAAAGTCTGTTTCTGCTTCTTACACATAGA
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA
AACTGACATTCCTTAAACTGAGAATTATAGATGGGGTCAAGAATCCC
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAAATGTGC
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT
GACCAATAAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA
AAATGATGA

FIG. 72B-1

302/498

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Leu Gly Ala Glu Tyr
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
His Lys Met Val Tyr Glu Asp Thr Leu Phe Pro Phe Ser Gly Glu Thr Val
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe

FIG. 72B-2

303/498

Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
 Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn
 Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln
 Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp
 Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu
 Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu
 Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
 Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
 Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr
 Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu
 Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu
 Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly
 Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn
 Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly
 Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly
 Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu
 Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp
 Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser
 Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
 Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser
 Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala
 Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg
 Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro
 Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu
 Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly
 Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp
 Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile
 Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
 Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln
 Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg
 Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys
 Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val
 Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe
 Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu
 Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn
 Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu
 Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile
 Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile
 Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro

FIG. 72B-3 304/498

Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu
Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr
Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser
Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro
Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu
Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys
Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu
Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu
Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile
Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu
Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg
Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp
Tyr Gly Met Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val
Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro
Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg
Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro
Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu
Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu
Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr
Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro
Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly
Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys
Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr
Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu
His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr
Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln
Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly
Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile

FIG. 72B-4

305/498

Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr
His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr
Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln
Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr

306/498

FIG. 73A

TCCACCTGTCCCCGAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG
GCGCGCCTGCTTCTCTGCGTCCTGGTTCGTGAGCGACTCCAAAGGCAGC
AATGAACTTCATCAAGTTCCATCGAACTGTGACTGTCTAAATGGAGGA
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC
CCAAAGAAATTCGGAGGGCAGCACTGTGAAATAGATAAGTCAAAAAC
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG
ACACCATGGGCGGGCCCTGCCTGCCCTGGAACCTCTGCCACTGTCTTTC
AGCAAACGTACCATGCCCACAGATCTGATGCTCTTCAGCTGGGCTGG
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGCGACCCCTGG
TGCTATGTGCAGGTGGGCTAAAGCCGCTTGTTCCAAGAGTGCATGGT
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT
TAAAATTTCAGTGTGGCCAAAAGACTCTGAGGCCCGCTTTAAGATTA
TTGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTGC GGCC
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTGCTCAA
GGCTTAACCTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGA AAAAC
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA
AGCTGATTTCCACCGGAGGTGTGTCAGCAGCCCCACTACTACGGCTCTG
AAGTACCCAGGAGGAAAATGCTGTGTGCTGACCCACAGTCAGTGAAACGA
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA
GGGTCCCAAGGAGGAAAACGGGCACCAACCGCTTCTTGCTGGTTGTC
ATTTTTGCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA
AGAT

307/498

FIG. 73B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

308/498

FIG.74A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAAATTGTCATCA
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGCGCTGCTG
GCACTGGCGGCCCTACTGCAGGGGGCCGTGTCCCTGAAGATCGCAGC
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTTCGTGTA
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT
GTCAGGTTCTTCTCCCGTTACAGAGGTCAGGGAGTTTGCCATTGTT
CCCCTGCATGCGGCCCGGGGACGCAGTAGCCGAGATCGACGCTCT
CTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAGGACG
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTC
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG
CTGAAGTGAGCAGCCCCCTCCCCACACCAGTTGAACTGCAG

309/498

FIG. 74B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu Leu Gln
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
Glu Val Met Leu Lys

310/498

FIG. 75A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG
CCCTGTGGATGCGCCTCCTGCCCTGCTGGCGCTGCTGGCCCTCTGGG
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGCTCAC
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA
GGTGGAGCTGGGCGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG
CAGCCCGCAGGCAGCCCCCACCCGCCCTCCTGCACCGAGAGAGA
TGAATAAAGCCCTTGAACCAGC

FIG. 75B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly
Pro Asp Pro Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

311/498

FIG. 76A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT
TTCTGTTCCCAATCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCT
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC
GGGCCAGGGTTCACCCACCACACGGCGGTCTTTGGGGTGGAGCCC
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCTG
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAACCCACAACA
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGCCTATATTTCTCT
GCTGGTGGCTCCAGTTCGGAACAGTAAACCCGTGTTCCGACTACTGTC
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC
ATGGAGAGCACAACATCAGGATTCTAGGACCCTGCTCGTGTACA
GGCGGGGTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT
AGACTCGTGGTGGACTTCTCTCAATTTCTAGGGGGAGCACCCACGTG
TCCTGGCCAAAATTGCGAGTCCCCAACCTCCAATCACTACCAACCTC
TTGTCTCCAATTTGTCTGGTTATCGCTGGATGTGTCTCGCGCGTTTT
ATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTGGTTC
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT
CAAGGAACCTCTATGTTTCCCTCTTGTGCTGTACAAAACCTTCGGAC
GGAAACTGCACCTGTATTCCCATCCCATCATCCTGGGCTTTCGCAAGA
TTCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA
GTGCCATTTGTGTCAGTGGTTCGACGGGCTTCCCCCACTGTTTGGCTTT
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT
TGAGTCCCTTTTACCTCTATTACCAATTTCTTTTGTCTTTGGGTATAC
ATTTGA

312/498

FIG. 76B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
Trp Val Tyr Ile

313/498

FIG. 77A

CGAACCCTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA
 CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCTGCTCTGCCTGC
 CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGC
 CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT
 TTGACACCTACCAAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG
 AAGTATTCATTCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG
 TCTATTCGACACCCCTCCAACAGGGAGGAAACACAACAGAAATCCAA
 CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA
 GCCCCTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG
 CGCCTCTGACAGCAACGCTCTATGACCTCCTAAAGGACCTAGAGGAAG
 GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCGGACT
 GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA
 CAACGATGACGCTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG
 GAAGGACATGGCAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCG
 CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG
 TGACCCCTCCCCAGTGCTCTCTCTGGCCCTGGAAGTTGCCACTCCAGT
 GCCCACCAGCCTGTCTCTAATAAAATTAAGTTGCATC

FIG. 77B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
 Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp
 Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
 Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
 Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr
 Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
 Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
 Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly
 Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
 Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

314/498

FIG. 78A

ATGTATTCCAATGTGATAGGAACTGTAACCTCTGGAAAAAGGAAGGT
TTATCTTTTGTCTTGTCTGCTCATTGGCTTCTGGGACTGCGTGACCTGT
CACGGGAGCCCTGTGGACATCTGCACAGCCAAGCCGCGGGACATTCC
CATGAATCCCATGTGCATTTACCGCTCCCCGGAGAAGAAGGCAACTG
AGGATGAGGGCTCAGAACAGAAGATCCCGGAGGCCACCAACCGGCG
TGCTGGGAACTGTCCAAGGCCAATTCCCGCTTTGCTACCACTTTCTA
TCAGCACCTGGCAGATTCCAAGAATGACAATGATAACATTTTCTGTCT
ACCCCTGAGTATCTCCACGGCTTTTGTCTATGACCAAGCTGGGTGCTG
TAATGACACCCTCCAGCAACTGATGGAGGTATTTAAGTTTGACACCAT
ATCTGAGAAAAACATCTGATCAGATCCACTTCTTCTTTGCCAAACTGAA
CTGCCGACTCTATCGAAAAAGCCAACAAATCCTCCAAGTTAGTATCAGC
CAATCGCCTTTTTGGAGACAAATCCCTTACCTTCAATGAGACCTACCA
GGACATCAGTGAGTTGGTATATGGAGCCAAGCTCCAGCCCCTGGACT
TCAAGGAAAAATGCAGAGCAATCCAGAGCGGCCATCAACAAATGGGTG
TCCAATAAGACCGAAGGCCGAATCACCGATGTCATTCCCTCGGAAGC
CATCAATGAGCTCACTGTTCTGGTGCTGGTTAACACCATTACTTCAA
GGGCTGTGGAAGTCAAAGTTCAGCCCTGAGAACACAAGGAAGGAAC
TGTTCTACAAGGCTGATGGAGAGTCTGTTTCAGCATCTATGATGTACC
AGGAAGGCAAGTTCCGTTATCGGCGCGTGGCTGAAGGCACCCAGGTG
CTTGAGTTGCCCTTCAAAGGTGATGACATCACCATGGTCTCATCTTG
CCCAAGCCTGAGAAGAGCCTGGCCAAGGTGGAGAAGGAACTCACCCC
AGAGGTGCTGCAGGAGTGGCTGGATGAATTGGAGGAGATGATGCTGG
TGGTCCACATGCCCCGCTTCCGCATTGAGGACGGCTTCAGTTTGAAGG
AGCAGCTGCAAGACATGGGCCTTGTGATCTGTTTCAGCCCTGAAAAA
TCCAAATCCCAAGGTATTGTTGTCAGAAGGCCGAGATGACCTCTATGTC
TCAGATGCATTCCATAAGGCATTTCTTGAGGTAAATGAAGAAGGCAG
TGAAGCAGCTGCAAGTACCGCTGTTGTGATGCTGGCCGTTGCTATAA
CCCCAACAGGGTGACTTTCAAGGCCAACAGGCCTTTCTGGTTTTAT
AAGAGAAAGTTCCTCTGAACACTATTATCTTCATGGGCAGAGTAGCCA
ACCTTGTGTTAAGTAA

315/498

FIG. 78B

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val Tyr Leu Leu
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser Pro Val Asp
Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys Ile Tyr Arg Ser
Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr
Asn Arg Arg Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Ile His
Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser
Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu
Thr Tyr Gln Asp Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe
Lys Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Ser Pro Glu
Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser
Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln
Val Leu Glu Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys
Pro Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
Trp Leu Asp Glu Leu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg
Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val Asp
Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu Gly Arg Asp Asp
Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser
Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys

316/498

FIG. 79A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCAG
AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCA
ATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCA
CTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAGA
GTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATGGG
GGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTT
ATTATCACAAATCTTAA

FIG. 79B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

317/498

FIG. 79C

ATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCAT
CAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCA
CCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCG
TGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACC
GCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCGCGGCG
TGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCAC
TCTGCCGCCGAGCACCCTGACTGCGGGGGTCCCAAGGACCACCCC
TTGACCTGTGATGACCCCGCTTCCAGGACTCCTCTCCTCAAAGGCC
CCTCCCCCAGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGAC
ACCCCGATCCTCC CACAATAA

FIG. 79D

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr
Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala
Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly
Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val
Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg
Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys
Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp
Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser
Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln

318/498

FIG. 80A

ATGCGTCCCCTGCGCCCCCGCGCCGCGCTGCTGGCGCTCCTGGCCTCG
CTCCTGGCCGCGCCCCCGGTGGCCCCGCGCGAGGCCCGCACCTGGT
GCAGGTGGACGCGGCCCGCGCGCTGTGGCCCCCTGCGGCGCTTCTGGA
GGAGCACAGGCTTCTGCCCCCGCTGCCACACAGCAGGCTGACCAG
TACGTCCTCAGCTGGGACCAGCAGCTCAACCTCGCCTATGTGGGCGCC
GTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCACTGGCTGCTGGA
GCTTGTCACCAACAGGGGGTCCACTGGACGGGGCCTGAGCTACAACT
TCACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCC
TCCCAGGGTTTGAGCTGATGGGCAGCGCCTCGGGCCACTTCACTGACT
TTGAGGACAAGCAGCAGGTGTTTTGAGTGGAAGGACTTGGTCTCCAGC
CTGGCCAGGAGATACATCGGTAGGTACGGACTGGCGCATGTTTCAA
GTGGAACCTTCGAGACGTGGAATGAGCCAGACCACCACTTTGACA
ACGTCTCCATGACCATGCAAGGCTTCTGAACTACTACGATGCCTGCT
CGGAGGGTCTGCGCGCCGCCAGCCCCGCTGCGGCTGGGAGGCCCC
GGCGACTCCTTCCACACCCACCGCGATCCCCGCTGAGCTGGGGCCTC
CTGCGCCACTGCCACGACGGTACCAACTTCTTCACTGGGGAGGCGGG
CGTGCGGCTGGACTACATCTCCCTCCACAGGAAGGGTGCGCGCAGCT
CCATCTCCATCCTGGAGCAGGAGAAGGTGCTGCGCAGAGTGGCGCG
CAGCTCTTCCCCAAGTTCGCGGACACCCCCATTTACAACGACGAGGCG
GACCCGCTGGTGGGCTGGTCCCTGCCACAGCCGTGGAGGGCGGACGT
GACCTACGCGGCCATGGTGGTGAAGGTCACTCGCGCAGCATCAGAACC
TGCTACTGGCCAAACCACTCCGCTTCCCTTCCGCTCCTGAGCA
ACGACAATGCCTTCTGAGCTACCACCCGACCCCTTCGCGCAGCGCA
CGCTCACCGCGCGCTTCCAGGTCAACAACACCCGCCCCGCGCACGTG
CAGCTGTTGCGCAAGCCGGTGCTCACGGCCATGGGGCTGCTGGCGCT
GCTGGATGAGGACGAGCTCTGGGCCGAAGTGTCGACGGCCGGGACCG
TCCTGGACAGCAACCACACGGTGGGCGTCTGGCCAGCGCCACCGC
CCCCAGGGCCCGGCCGACGCTGGCGCGCCGCGGTGCTGATCTACGC
GAGCGACGACACCCGCGCCACCCCAACCGCAGCGTTCGCGGTGACCC
TGCGGCTGCGCGGGTGCCCCCGGGCCGGGCTGGTCTACGTCACG
CGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGCGCGG
CCTGGGCGCGCCGCTTCTCCCCACGGCAGAGCAGTTCGGGCGCATGC
GCGCGGCTGAGGACCCGGTGGCCGCGGGCGCCCGCCCTTACCCGCC
GGCGGCCGCTGACCTGCGCCCCGCGCTGCGGCTGCCGTGCTTTTG
CTGGTCAAGTGTGTGCGCGCCCGAGAAGCCGGGAGGTAC
GCGGCTCCGCGCCCTGCCCTGACCAAGGGCAGCTGGTTCTGGTCTG
GTCGGATGAACACGTGGGCTCCAAGTGCCTGTGGACATACGAGATCC
AGTTCTCTCAGGACGGTAAGGCGTACACCCGGTCAGCAGGAAGCCA
TCGACCTTCAACCTTTGTGTTTACGCCAGACACAGGTGCTGTCTCT
GGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCGACCAAGCC
CTTCTCGGACCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCC
CCCATCCCCGGGCAATCCATGA

319/498

FIG. 80B

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu
Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val Gln Val Asp Ala Ala
Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu
Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala
Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu
Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His
Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu
Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val
Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly
Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp
Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys
Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
Phe His Thr Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp
Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His
Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln
Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala
Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala
Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr
Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro
His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu
Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala
Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro
Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu
Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp
Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg
Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu
Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala
Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln
Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr
Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro
Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr
Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro
Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

320/498

FIG. 81A

ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCCT
TCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACT
GGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGG
AGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCAGATTCTGC
ATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGA
AGGCTGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTG
GATGGCTCCCCAAAGAGATTGAGAAGGCAGACTTCAGGCAGACCCTC
AGCGCTTCCTCATGGGATTGCCAGCTAGCTAATTATGTTACAGCA
AAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGC
GCAGGCTTCCCTGGGAGTTTGGATACTACGACATTGATGCCAGACC
TTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGT
GACAGTTTGAAAAATTTGGCAGATGGTTATAAGCACATGTCCTTGGCC
CTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCTCTT
TATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGACAGTAC
TGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAAGT
ATAAAGAGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTT
GATGTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGAT
TGGCAACTTTGGCCTCAGCTGGAATCAGCAAGTAACTCAGATGGCCCT
CTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACA
CATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGC
CATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGG
GAGACAACCTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGG
GCTGTAGCTATGATAAAACCGCAGGAGATTGGTGGACCTCGCTCTTAT
ACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCTGCC
TGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTCTAT
GAATGGACTTCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGT
TTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAGGACTTACT
TTAA

321/498

FIG. 81B

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe
Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala
Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met Cys Asn Leu Asp
Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys Leu Phe Met Glu Met Ala Glu
Leu Met Val Ser Glu Gly Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp
Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln
Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys
Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly Ser Phe
Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys
Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn Leu Ala Asp Gly Tyr Lys His
Met Ser Leu Ala Leu Asn Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro
Leu Tyr Met Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu
Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro Gly Gly Trp
Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu Ser Trp Asn Gln Gln
Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp
Leu Arg His Ile Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala
Ile Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn
Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser Leu Gly Lys
Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu Leu Pro Val Lys Arg Lys
Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr
Val Leu Leu Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu

322/498

FIG. 82A

ATGGCGCCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGACTGGAGCT
CTGGGCTGCGGCGCACGCCTTGCCCGCCAGGTGGCATTACACCCTA
CGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG
GACAGCACATACCCCAGCTCTGGAACCTGGGTCCCCGAGTGCTTGAG
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACTCAAGCCTGCAC
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG
TGCCGCCCGGGCTTCGGCGTGGCCAGACCAGGAACCTGAAACATCAGA
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC
ATCCACGGATATTTCAGAGCCCCACCAGATCTGTAACGTGGTGGCCAT
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCACGCCAGTGTC
ACACGATCCCAACACACGCAGCCAACTCCAGAACCCAGCACTGCTCC
AAGCACCTCCTTCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAACGTGTGCATCATGAC
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC
CTCACTTGCCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCACTCGGAACACAGC
CACAGGCCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCGGGC
CAGCACCGGGAGCTCAGATTCTTCCCTGGTGGCCATGGGACCCAGG
TCAATGTACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT
CACAGTGTCTCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC
AGCCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCTTCTCCAAGGA
GGAATGTGCCTTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGG
GGAGCACCGAAGAGAAGCCCCCTGCCCTTGGAGTGCCTGATGCTGGG
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTCTGATGCCAAGG
TGGGCTGAGCCCTGGCAGGATGACCTGCGAAGGGGCCCTGGTCTT
CCAGGC

323/498

FIG. 82B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Leu Asp Arg
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
Asp Ala Gly Met Lys Pro Ser

324/498

FIG. 83A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 83B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
Gly Thr Leu Val Thr Val Ser Ser

325/498

FIG. 84A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ser

FIG. 84B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

326/498

FIG. 85A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA
 GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTTCGTTGGCTCAAGC
 ATCCACTGGTATCAGCAAAGAACAATGGTTCTCCAAGGCTTCTCATA
 AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC
 AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT
 GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC
 ACGTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA
 GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT
 CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAACTGGG
 TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA
 TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
 AGGTTACCATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA
 ATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCCAGG
 AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC
 ACAGTCTCC

FIG. 85B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val
 Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln
 Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly
 Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
 Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro
 Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly
 Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
 Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr
 Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg
 Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

327/498

FIG. 86A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTC
GGTTCCACTGGTGACGTCAAGGCGAGGGCCCCGGAGCCTGCGGGGCAG
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC
TGCTGGTCCGCCACTGCGTGCCCTGCGGGCTCCTGCGCACGCCGCGGC
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG
CCGCAGGAGTCGGTGGGCGCGGGGGCCGCGCAGGCGGCGGTGACACA
AACTCACACATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGA
CCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGACGTGAGCCACGA
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGC
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA
CCGTGTGGTCAGCGTCCTCACCCTGTCACCAGGACTGGCTGAATGG
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACG
CCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
CCCTGTCTCCCGGAAATGA

328/498

FIG. 86B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

329/498

FIG. 87

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
 Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
 Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
 Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

FIG. 88

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys
 Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
 Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe
 Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr
 Leu Val Thr Val Ser Ala

FIG. 89

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

FIG. 90

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
 Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
 Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 Thr Leu Val Thr Val Ser Ser

330/498

FIG. 91

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Thr Leu Thr Ile Ser
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 Ser Phe Asn Arg Gly Glu Cys

FIG. 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
 Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
 Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

331/498

FIG. 93A

ATGGATTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA
GTCATAATGTCCAGAGGGCAAATIGTTCTCTCCAGTCTCCAGCAATC
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCCAGGGCCAG
CTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGATCCTC
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC
TGTTGCTTCAGTGCCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT
GGACTAGTAACCCACCCACGTTCTGGAGGGGGGACCAAGCTGGAATC
AAA

FIG. 93B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

332/498

FIG. 94A

ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG
CCTGGGGCCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATT
ACCAGTTACAATATGCACTGGGTAAAACAGACACCTGGTCGGGGCCT
GGAATGGATTGGAGCTATTATCCCGGAAATGGTGATACTTCCTACAA
TCAGAAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 94B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ala

333/498

FIG. 95A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAAATAAAA
AAAATTAGTCAGCCATGCATGGGCGGAGAATGGGCGGAACCTGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTG
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCACAGAATTAATTTCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGGCC
ATTGACGTCATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATTGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCT
TATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTACATCGTA
TTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGTGGATAGC
GGTTTGACTCAGGGGATTTCGAAGTCTCCACCCCATTTGACGTCAATG
GGAGTTTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGGTGACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCAGAGATCTCTCACCATGAGGGTCCCCGCTCAGCTCT
GGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGATGGTACCAA
GGTGAAATCAAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCT
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAAGTCAACC
ATCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAG
TGTTGAATTGATCCGTTAACGGTTACCAACTACCTAGACTGGATTG
GTGACAACATGCGGCGTGATATCTACGTATGATCAGCCTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCCCGCTGCTTCT
TGACCCTGGAAGGTGCCACTCCCCTGTCCTTTTCTAATAAAATGAGG
AAATTGCATCGCATTTGTTCTGAGTAGGTGTCATTCTATTCTGGGGGGTG
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAAATGACG
GCATGCTGGGGATGCGGTGGGCTCTATGGAACCACTGGGGCTCGAC
AGCTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGC
CCGCTTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTACTT
GGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT
TTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCAGGGGA
TTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTGTTTGGCAC

334/498
FIG. 95B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG
ACGCAAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCCTCACATTACAGTGATCAGCACTGAACACAGACCC
GTCGACATGGGTTGGAGCCTCATCTTGCTTCTCCTTGTCGCTGTTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC
CCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA
TGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGCTAGTCTTC
CTCTTCCCCCAAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAGC
GTCCTACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCCAACAAGCCCTCCAGCCCCATCGAGAAAACCA
TCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAGGAACAGGTACGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGGAGAAACAACACAGACGCCTCCCGTGTCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTGCTG
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTGGCCCTCCCCCGTGCCTTCCTTGA
CCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGG
TGGGCGAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACCAAGCTGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTGTCTTCTCAATTCTTATTGTCATA
ATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTGAGTAGTTGAT
TGAGCAAAATGCGTTGGCAAAAAGGATGCTTGAAGACAAATAGCAGGCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGTGTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAAATATGCTT
GTCATACCCGAAGCCTGATTCCGTAGAGCCACACCTTGTTAAGGGCC
AATCTGCTACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

335/498

FIG. 95C

GCTGCGATTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAACTGCAT
CGTCGCCGTGTCCAAAAATATGGGGATTGGCAAGAACGGAGACCTAC
CCTGGCCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC
ACAACTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAG
GAAAACCTGGTTCTCCATTCTTGAGAACATCGACCTTTAAAGGACA
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACACCACGAGGA
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT
CTTTGTGACAAGGATCATGCAGGAATTTGAAAAGTGACACGTTTTTCCC
AGAAATTGATTTGGGGAAATATAAACTTCTCCAGAATACCCAGGCG
TCCTCTCTGAGTCCAGGAGGAAAAAGGCATCAAGTTATAAGTTGAA
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTCAAGTTCTCTGC
TCCCCTCCTAAAGTCATGCATTTTATAAGACCATGGGACTTTTGCTG
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTGT
TTGCCCTCCCCCGTGCTTCTTGACCTGGAAGGTGCCACTCCAC
TGTCTTTTCTCATAAATAAGGAAATTCATCGCATGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT
ATGGAACCAAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT
ATTTGCATAATTGAAAAAAGGAAAAATTAATTTAACACCAATTCA
GTAGTTGATTGAGCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACA
GTGTTCTCTGCACAGATAAGGACAAACATTATTAGAGGGAGTACCC
AGAGCTGAGACTCCTAAGCCAGTGAGTGGCACAGCATTTAGGGAGA
AATATGCTTGTCATCACCGAAGCCTGATTCGCTAGAGCCACACCTGG
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGCGAGGACGAGG
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAA
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC
GGCTATGACTGGGACAAACAGACAATCGGCTGCTCTGATGCCGCCGT
GTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGA
CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGACGCGCGGCTAT
CGTGGCTGGCCACGACGGGCGTTCTTGGCGCAGCTGTGCTCGACGTTG
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG
CAGGATCTCCTGTCTATCTACCTTGCTCCTGCCGAGAAAGTATCCATC
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
CCATTGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCG
GATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATC
AGGGGCTCGCGCCAGCCGAACCTGTTCCGCAAGGCTCAAGGCGCGCATG
CCCACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG

336/498

FIG. 95D

AATATCATGGTGGAAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGT
GCTTACGGTATCGCCGCTTCCGATTTCGACGCGCATCGCCCTTCTATC
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGAC
CGACCAAGCGACGCCCCAACCCTGCCATCAGGAGATTTTCGATTCCACCG
CCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTCCGGGACGCCG
GCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCC
ACCCCAACTTGTTTATTGACGCTTATAATGGTTACAAATAAAGCAATA
GCATCACAATTTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTT
GTGGTTTGTCCAAACTCATCAATCTATCTTATCATGTCTGGATCGCGG
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC
TGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGG
AGCATAAAGTGTAAGCCCTGGGGTGCCCTAATGAGTCGATTAACAC
ATTAATTGCGTTGCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTC
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
TGCGTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGTTCGCGCTC
GGTCGTTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAGGCGGTAA
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGC
TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATC
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC
CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCCTGTCCGACC
CTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG
GCGCTTCTCAATGTCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
GTTCTCGTCCAGCTGGGCTGTGTACGAACCCCCCGTTACGCCCCGAC
CGCTGCGCCTTATCCGGTAACCTATCGTCTTGAGTCCAACCGGTAAGA
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTGATCCGGCAAA
CAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTTCGAAGCAAGATT
ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC
GGGCTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGG
TCATGAGATTATCAAAAAAGGATCTTCACTAGATCCTTTTAAATTA
AATGAAGTTTTAAATCAATCTAAAGTATATAGATAAACTTGGTCTG
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC
TATTTCTGTTATCCATAGTTGCCTGACTCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC
GAGACCCACGCTACCGCTCCAGATTTATCAGCAATAAACACGCCA
GCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCTC
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCG

337/498

FIG. 95E

CAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTACAGGCATCGTGG
TGTCACGCTCGTCGTTTGGIATGGCTTCATTCAGCTCCGGTTCCCAAC
GATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTT
AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTG
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC
ATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCA
GCATCTTTTACTTTACCCAGCGTTTCTGGGTGAGCAAAAACAGGAAGG
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAATGTTGAA
TACTCATACTCTTCTTTTCAATATTATTGAAGCATTATCAGGGTTA
TTGTCTCATGAGCGGATACATATTTGAATGTATTAGAAAAATAAAACA
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

338/498

FIG. 96A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAAGTGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAAGTGA
CACACATTCCACAGAAATTAATCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCT
TATGGGACTTTCTACTTGGCAGTACATCTACGTTATAGTCAATCGTAA
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATACC
GGTTTGACTACGCGGATTTCCAAGTCTCCACCCCATTGACGTCAATG
GGAAGTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAAATGTCGTA
ACAACCTCCGCCCATTTGACGCAAAATGGGCGGTAGCCGCAATAGGGA
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCACAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT
CAGCTTCTCTGTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT
TGTTCTCTCCCACTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA
GGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATCCACT
GGTTCCAGCAGAAGCCAGGATCCTCCCCCAAACCTGGATTTATGCCA
CATCCAACCTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGT
CTGGGACTTCTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCAGCAGCA
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCC
TCTGTTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
CAGTGGAAGGTGGATAACGCCCTCCAATCGGTAAGTCCCAGGAGAG
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC
TGCGAAGTCAACCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT
CAACAGGGGAGAGTGTGAATTCAGATCCGTTACCGTTACCAACTA
CCTAGACTGGATTCTGTGACAACATGCGGCCGTGATATCTACGTATGAT
CAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTC
CCCCGTGCCTTCTTGACCTGGAAGGTGCCACTCCCACTGTCTTTCC

339/498
FIG. 96B

TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA
GCTGGGGCTCGACGCTATGCCAAGTACGCCCCCTATTGACGTCAATG
ACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT
GGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTTG
ACTACGGGGATTTCCAAAGTCTCCACCCCATTGACGTCAATGGGAGTT
TGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACT
CCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC
TATATAAGCAGAGCTGGGTACGTCTCACATTCAGTGATCAGCACTGA
ACACAGACCCGTGCACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT
CGCTGTTGTACGCGTGTCTGTCCAGGTACAACCTCAGCAGCAGCTGG
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAACAGA
CACCTGGTCCGGGCTGGAATGGATTGGAGCTATTTATCCCGGAAAT
GGTGATACCTTCTACAATCAGAAGTCAAAGGCAAGGCCACATTGAC
TGCAGACAAATCCTCCAGCACAGCCTACATGCAAGCTCAGCAGCTGA
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCAAC
GTCTCTGCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC
TCCTCCAAGAGCACCTCTGGGGGCAAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGCG
CCCTGACCAGCGGCGTGCACACCTTCCCGGTGTCTACAGTCTCTAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCAACACC
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGCAAAAACCTCACAC
ATGCCCCACCGTGCCAGCACCTGAACTCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCC
TGAGGTCAACATGTCGTGGTGGTGGAGCTGAGCCACGAAGACCTGAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGAGTATGCGCAAG
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCTCACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCC
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAGGTGACACCCT
GCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCGTACCT
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
AGCAATGGGACGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGTCT
GGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGCTTCTCATGTCTCCGTGATGCGATG
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGT

340/498

FIG. 96C

GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC
TTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTG
ACCCCTGGAAGGTGCCACTCCCACTGTCTTTCTTAATAAAATGAGGAA
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGG
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC
ATGCTGGGGATGCGGTGGGCTCTATGGAACCACTGGGGCTCGACAG
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTCAT
AATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGA
TTGAGCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCT
GCACAGATAAGGACAAACATTATTTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCTACACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTCGCATTCG
CGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC
CCCGCTGCCATCATGGTTTCGACCATTTGAAGTGCATCGTCGCGGTGTC
CAAAATATGGGATTGGCAAGAACGGAGACCTACCTGGCCCTCCGCT
CAGGAACGAGTTCAAGTACTTCCAAAGAATGACCACAACCTTCTCAG
TGGAAGGTAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGTTC
TCCATTCTGAGAAGAAATCGACCTTTAAAGGACAGAATTAATATAGTT
CTCAGTAGAGAACTCAAAGAACCACACGAGGAGCTCATTTTCTTGC
CAAAAGTTTGGATGATGCCCTTAAGACTTATGGAACACCGGAATTGG
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCGTTTACC
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG
ATCATGCAGGAATTTGAAAAGTGACACGTTTTTCCAGAAATTGATTG
GGGAAATATAAACTTCTCCAGAATACCCAGGCGTCTCTGA
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCCCTCTAA
AGCTATGCATTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA
GCCTCGACTGTGCCCTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCC
CCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACCTGCTTCTTA
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCTTCTAT
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCACT
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTATTGTCATAATG
AGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGATTGA
GCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCTGCA
CAGATAAGGACAAACATTATTTCAGAGGGAGTACCCAGAGCTGAGACT
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTG
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG

341/498
FIG. 96D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTG
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC
AGCGCAGGGGCGCCCGTTCTTTTGTCAAAGACCGACCTGTCCGGTGC
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA
CGACGGGCGTTCTTGCAGCTGTGCTCGACGTTGTCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG
TCATCTCACCTTGCTCCTGCGGAGAAAGTATCCATCATGGCTGATGCA
ATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAC
CAAGCGAAACATCGCATCGAGCGAGCACGTA CT CGGATGGAAGCCGG
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC
CAGCCGAAC TGTTCCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAG
GATCTCGTCGTGACCCATGGCGATGCCGTGCTTGCCGAATATCAGCCAC
GAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTG
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
AGAGCTTGGCGGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTAT
CGCCGCTCCGATTCTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA
GTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGCA
GCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGA
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTT
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTGTCCAA
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATGTT
TATCCGCTTACAAATTTCCACACAACATACGAGCCGGAAGCATAAAGTG
TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
GCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCA
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGC
GCTTCTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCCGGCT
GCGGCGAGCGGTATCAGCTCACTCAAGGCGGTAATACGGTTATCCA
CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC
ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACACGGCTTTC
CCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTAC
CGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAA
GCTGGGCTGTGTGCACGAACCCCGGTTACGCCGACCGCTGCGCCTT
ATCCGGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

342/498

FIG. 96E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGC
TGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAA
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC
TCAGTGGAAACGAAAACCTCACCTAGATCCTTTAAATAAAAATGAAGTTTAA
AAAAAGGATCTTCACCTAGATCCTTTAAATAAAAATGAAGTTTAA
ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
CTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC
ACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCG
AGCGCAGAAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTA
ATTGTTGCCGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGT
TTGGTATGGCTTCATTAGCTCCGGTTCCCAACGATCAAGGCGAGTTA
CATGATCCCCCATGTTGTGCAAAAAAGCGTTAGCTCCTTCGGTCTC
CGATCGTTGTCAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTA
TGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCT
TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
TGCGGCGACCGAGTTGCTCTTGCCCGCGTCAATACGGGATAATACC
GCGCCACATAGCAGAACTTTAAAAAGTGCTCATCATTGGAAAACGTTCT
TCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTTCG
ATGATACCCACTCGTGCACCCAACCTGATCTTCAGCATCTTTTACTTTCA
CCAGCGTTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAA
AAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCT
TTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGACGG
ATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTCCGC
GCACATTTCCCGAAAAAGTGCCACCT

343/498

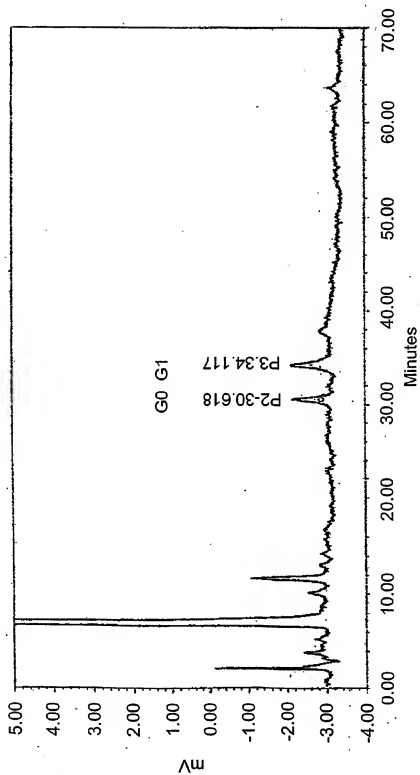


FIG. 97A

344/498

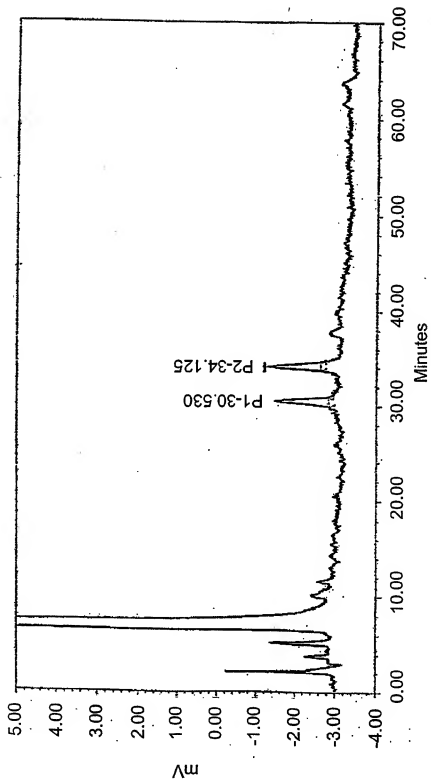


FIG. 97B

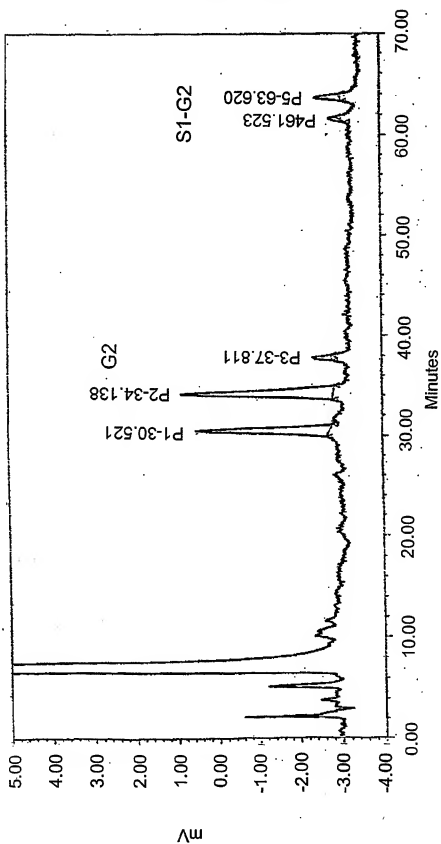


FIG. 97C

346/498

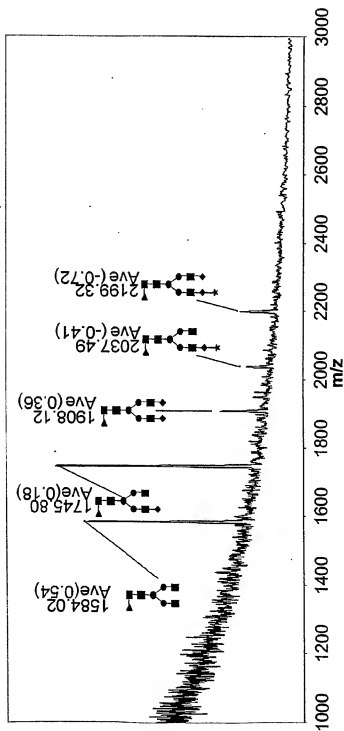


FIG. 98A

347/498

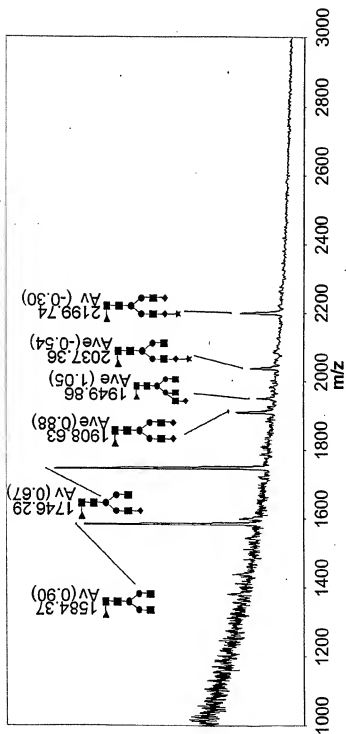


FIG. 98B

348/498

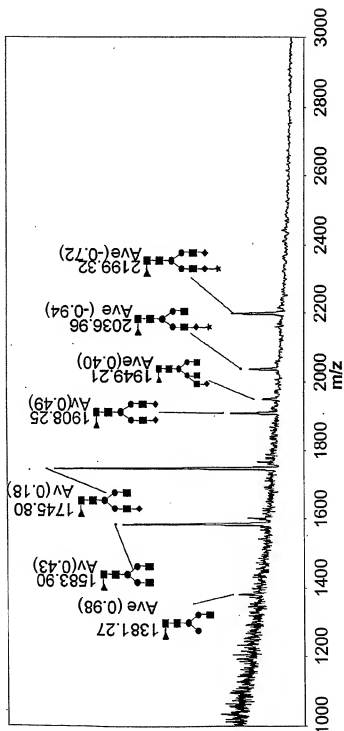


FIG. 98C

349/498

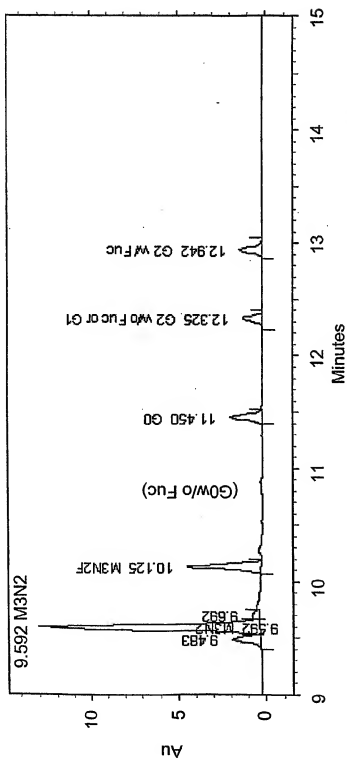


FIG. 99A

350/498

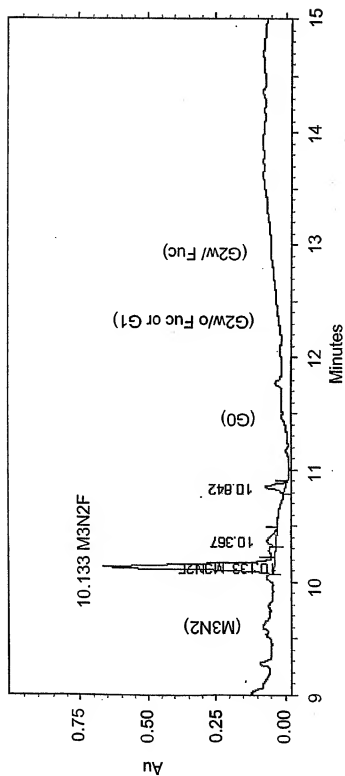


FIG. 99B

351/498

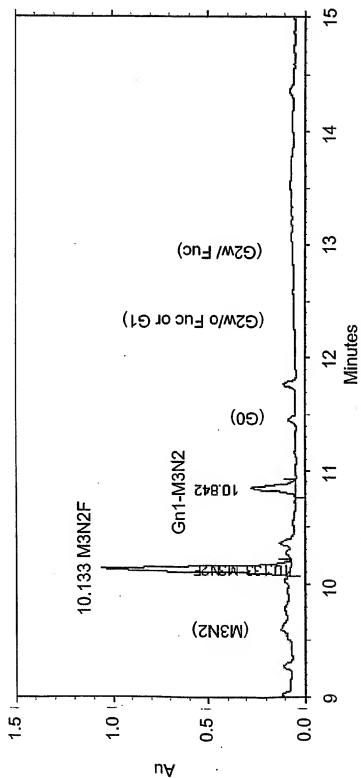


FIG. 99C

352/498

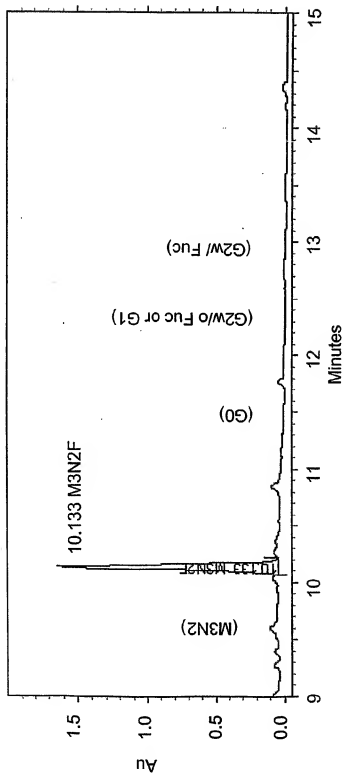


FIG. 99D

353/498

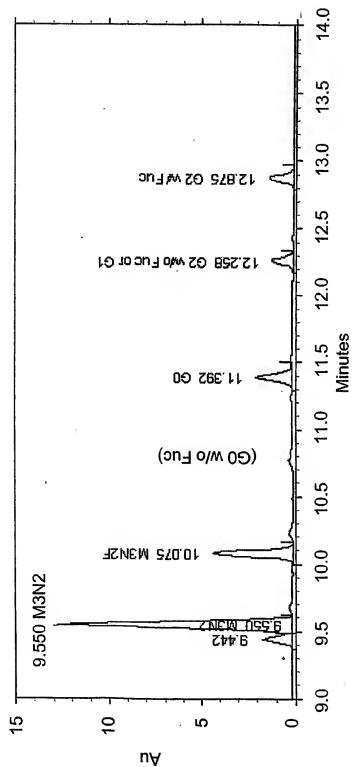


FIG. 100A

354/498

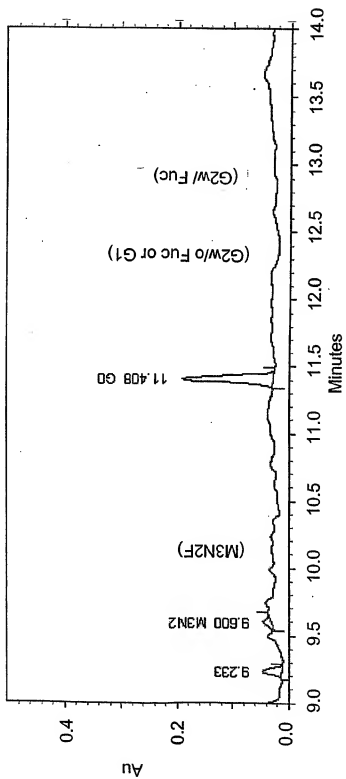


FIG. 100B

355/498

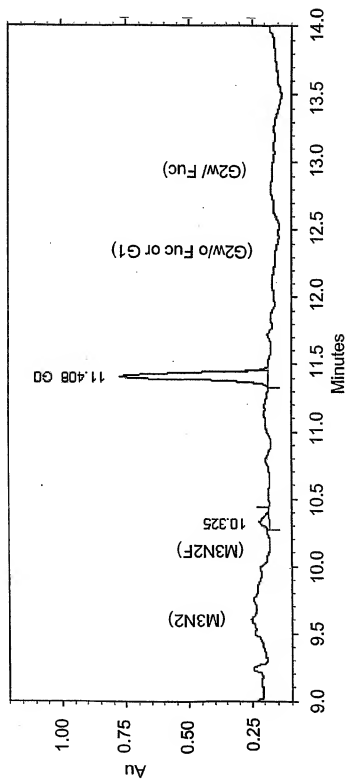


FIG. 100C

356/498

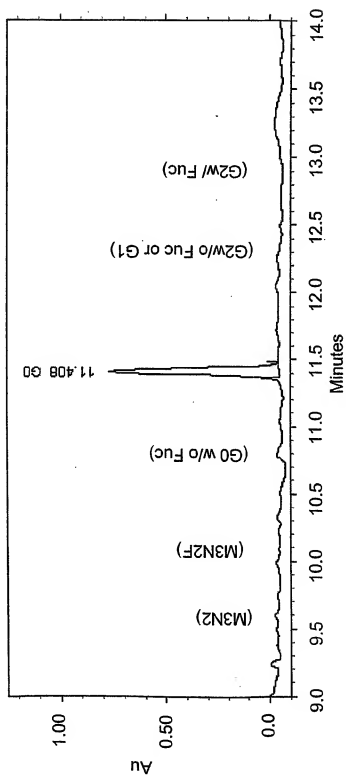


FIG. 100D

357/498

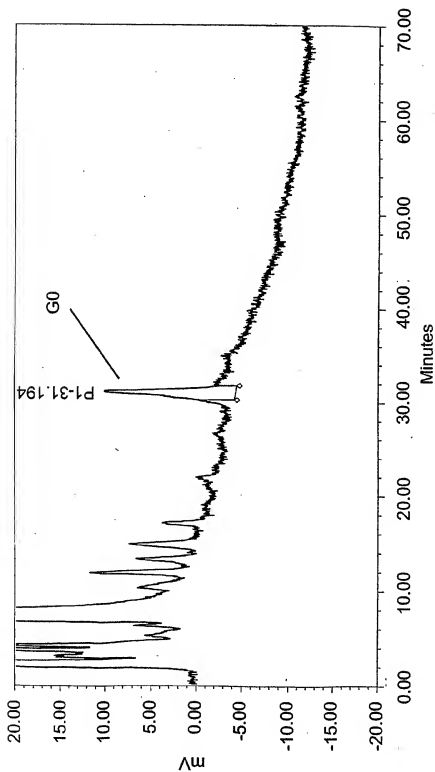


FIG. 101A

358/498

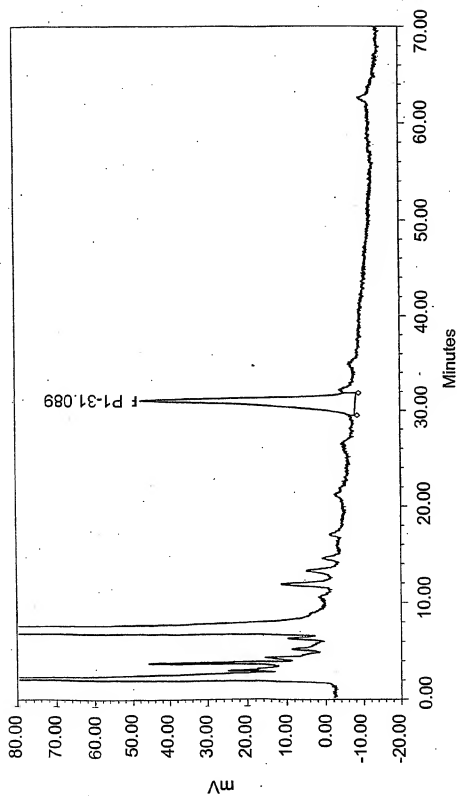


FIG. 101B

359/498

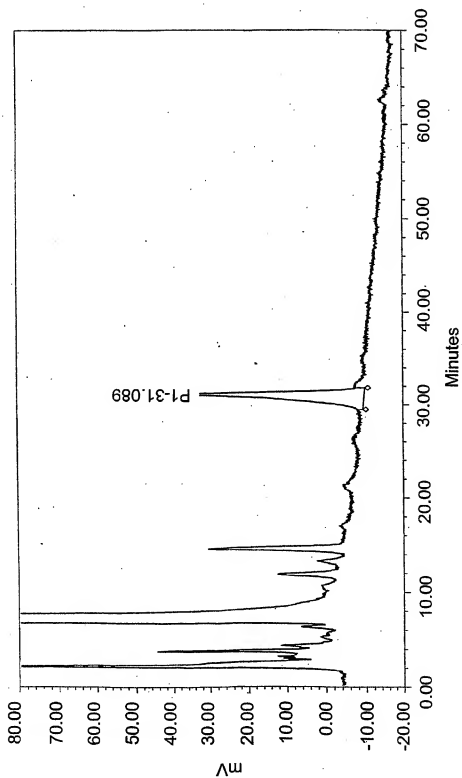


FIG. 101C

360/498

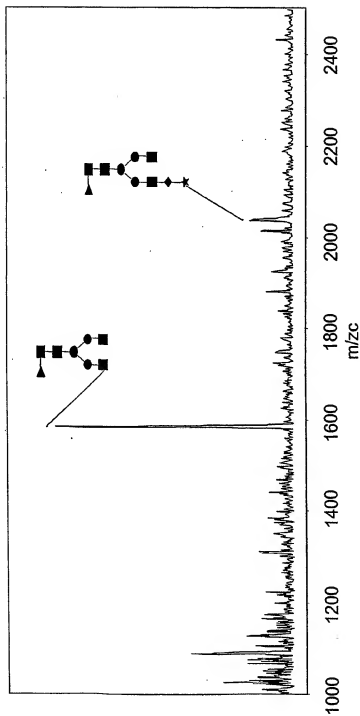


FIG. 102A

361/498

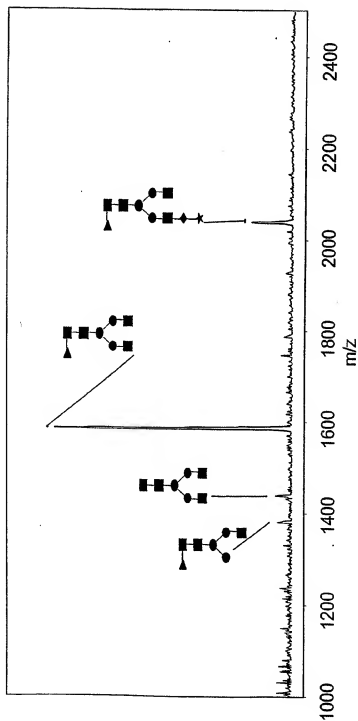


FIG. 102B

362/498

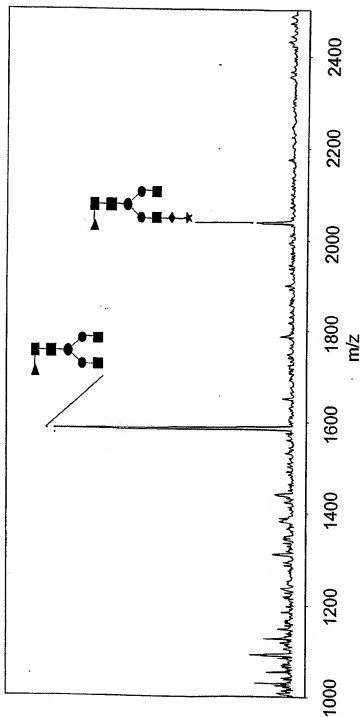


FIG. 102C

363/498

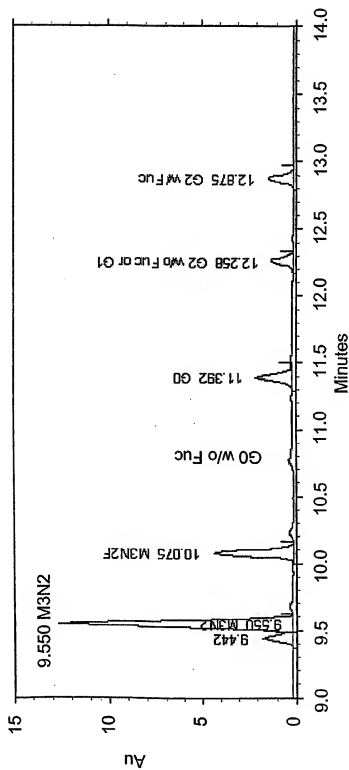


FIG. 103A

364/498

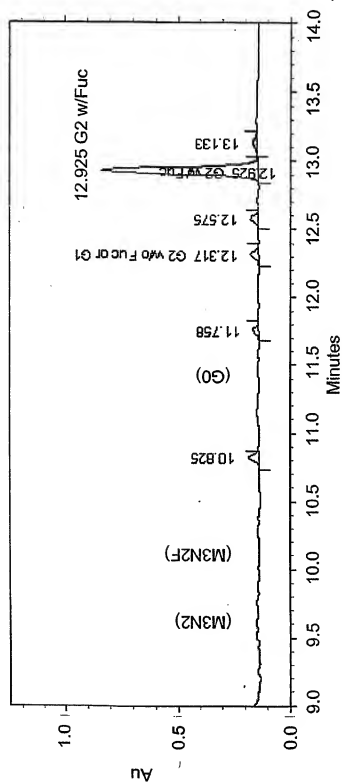


FIG. 103B

365/498

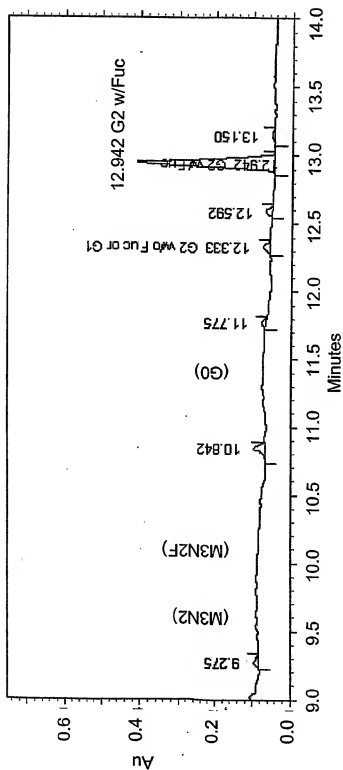


FIG. 103C

366/498

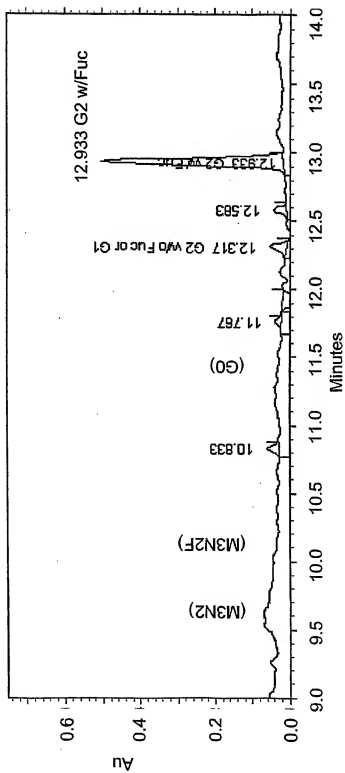


FIG. 103D

367/498

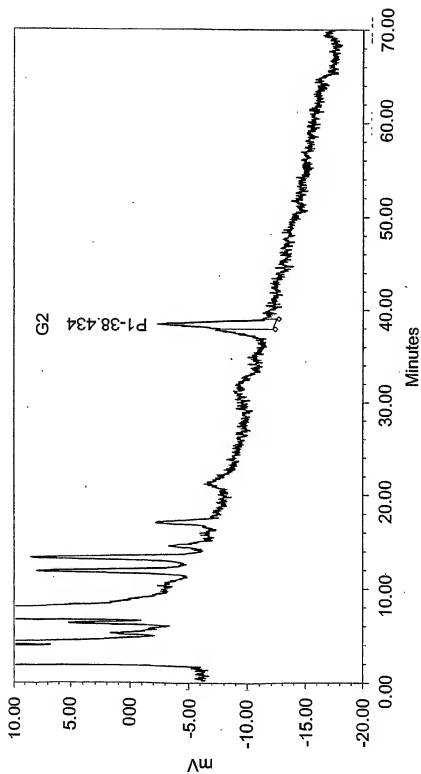


FIG. 104A

368/498

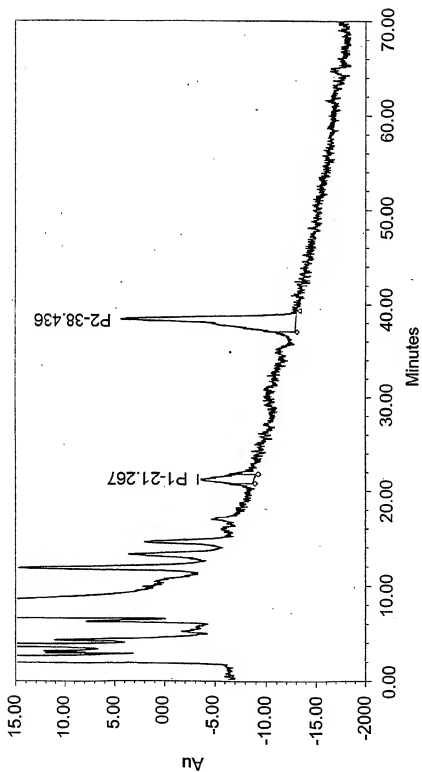


FIG. 104B

369/498

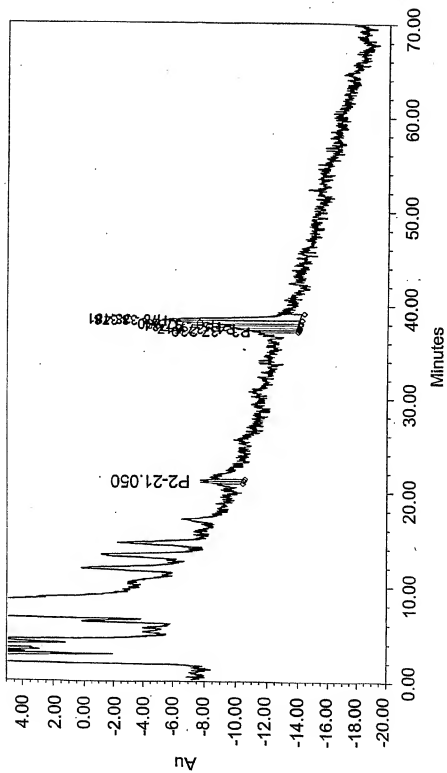


FIG. 104C

370/498

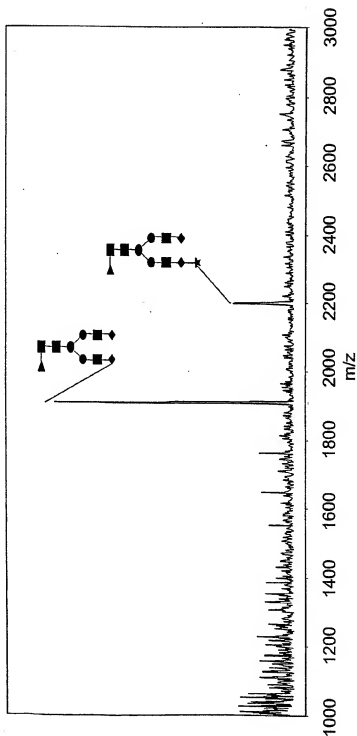


FIG. 105A

371/498

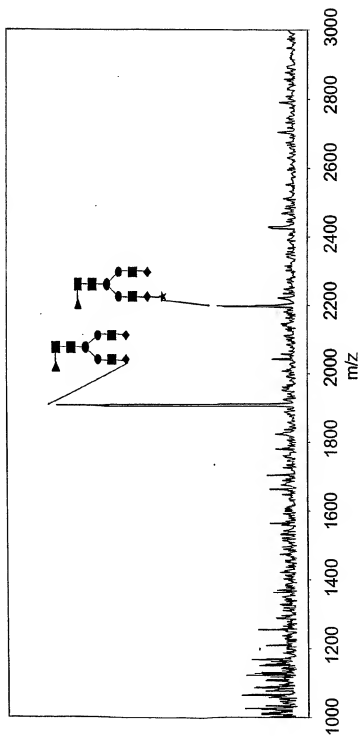


FIG. 105B

372/498

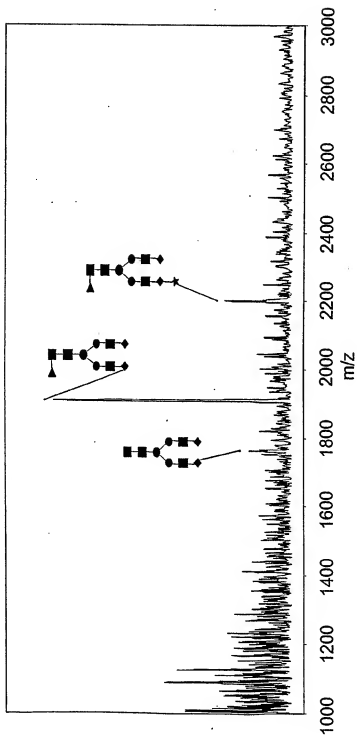


FIG. 105C

373/498

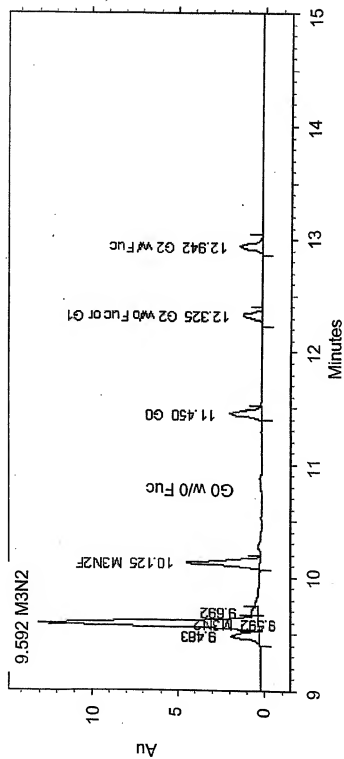


FIG. 106A

374/498

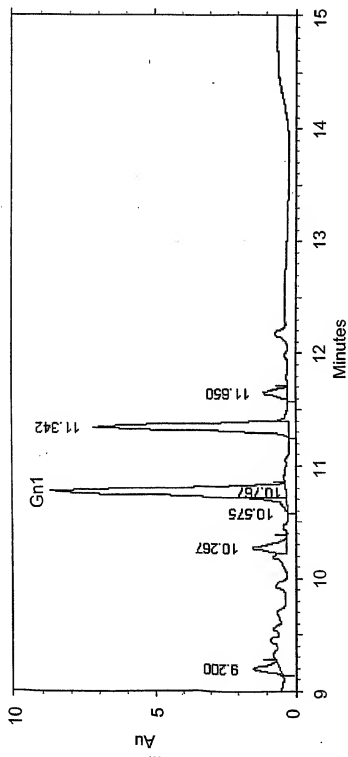


FIG. 106B

375/498

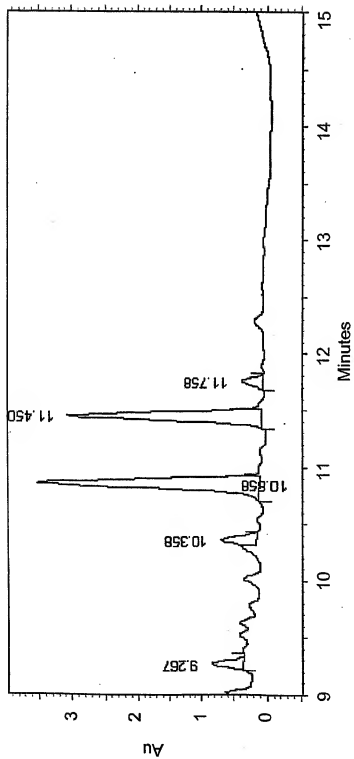


FIG. 106C

376/498

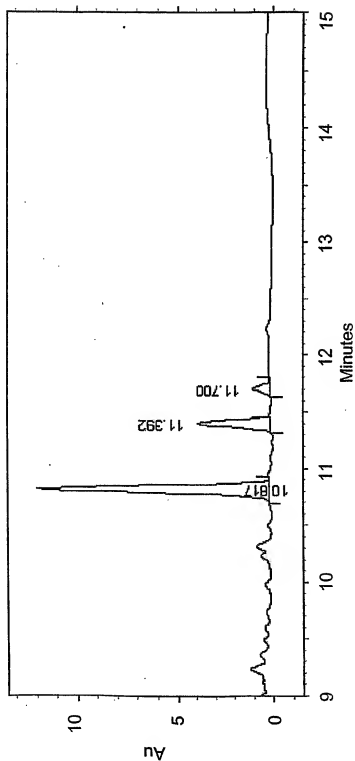


FIG. 106D

377/498

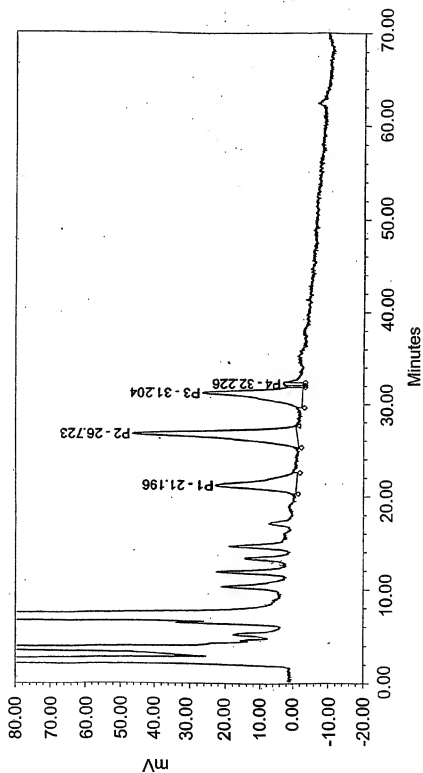


FIG. 107A

378/498

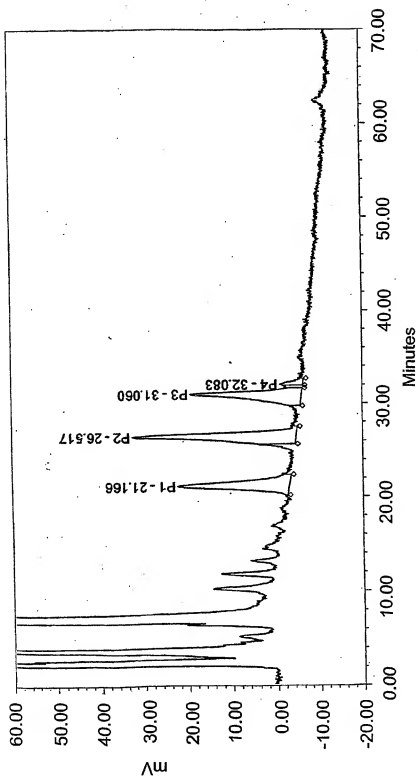


FIG. 107B

379/498

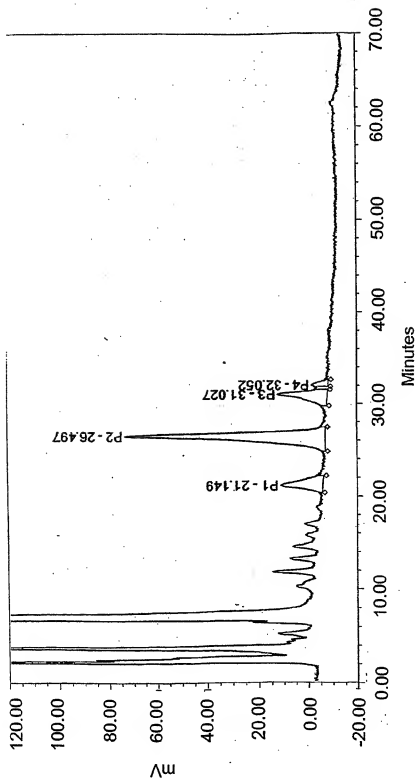


FIG. 107C

380/498

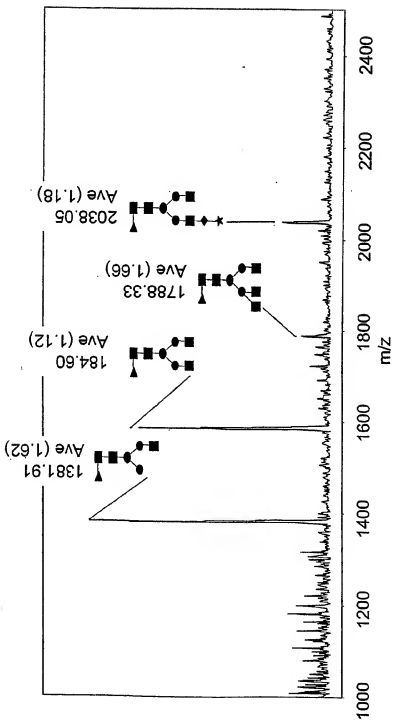


FIG. 108A

381/498

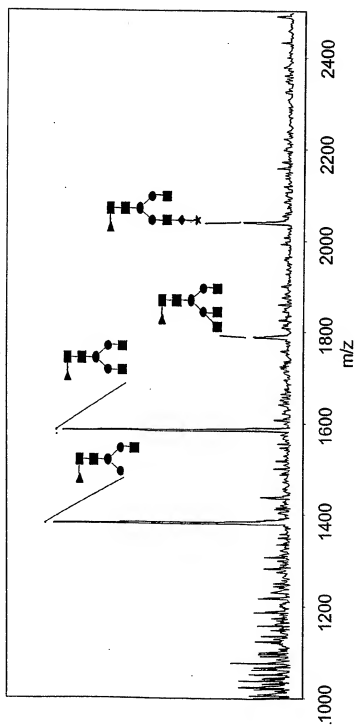


FIG. 108B

382/498

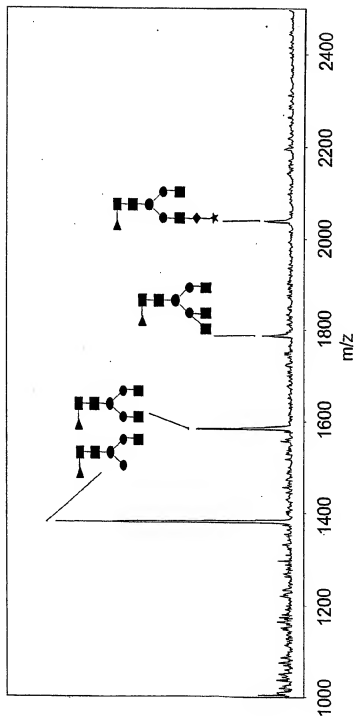


FIG. 108C

383/498

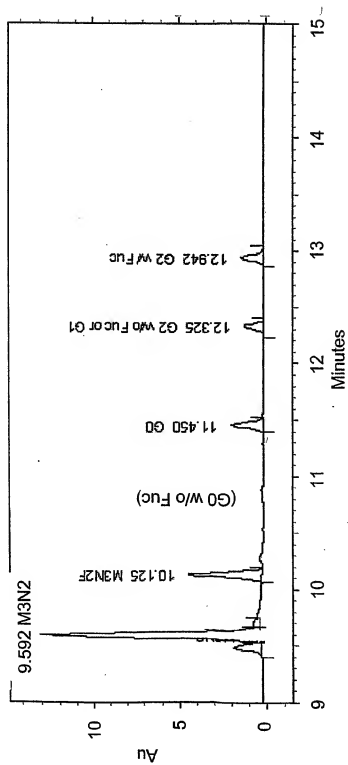


FIG. 109A

384/498

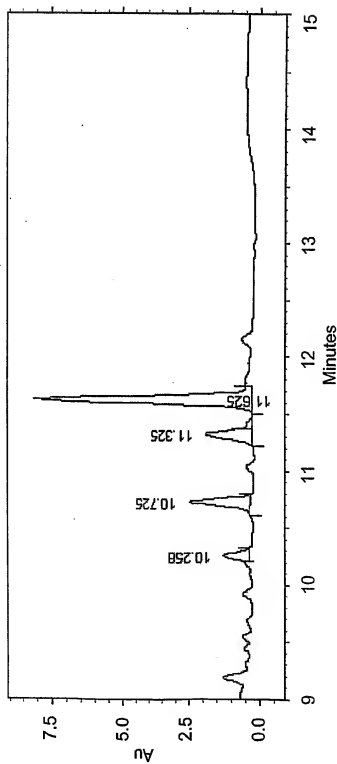


FIG. 109B

385/498

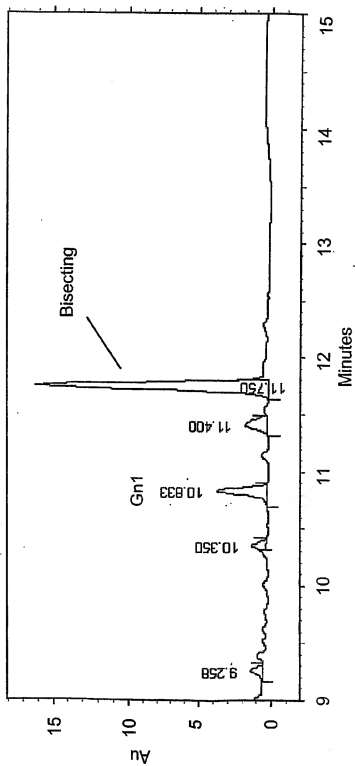


FIG. 109C

386/498

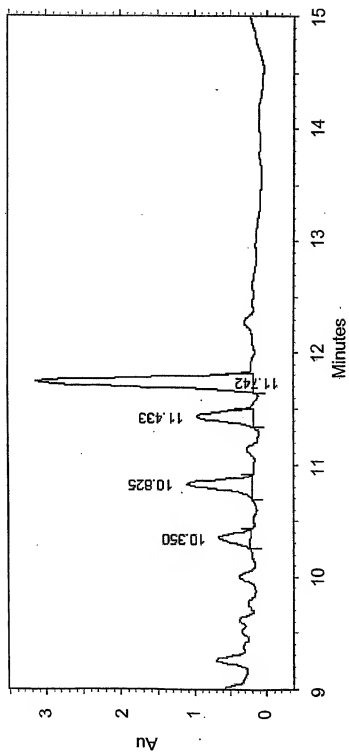


FIG. 109D

387/498

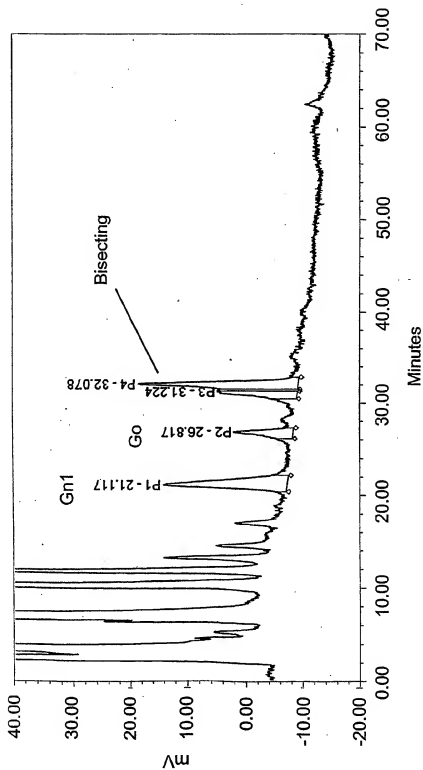


FIG. 110A

388/498

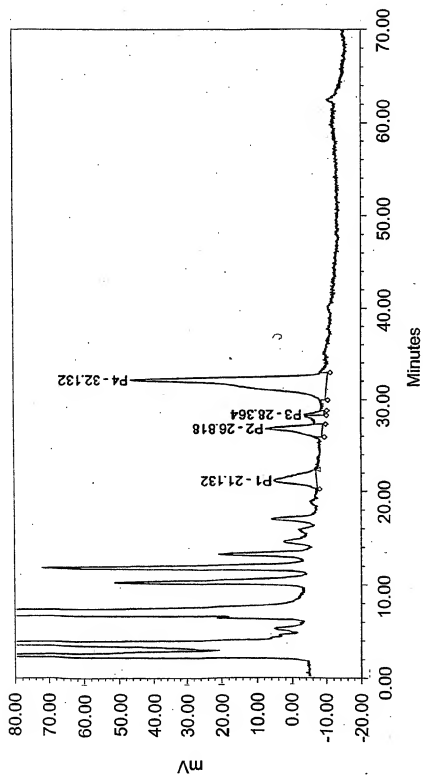


FIG. 110B

389/498

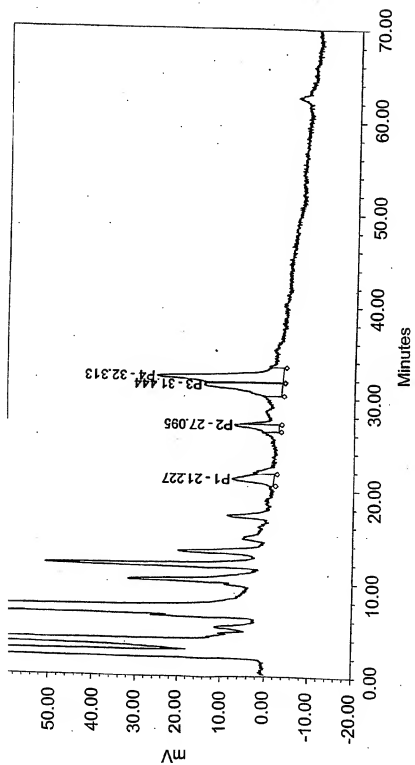


FIG. 110C

390/498

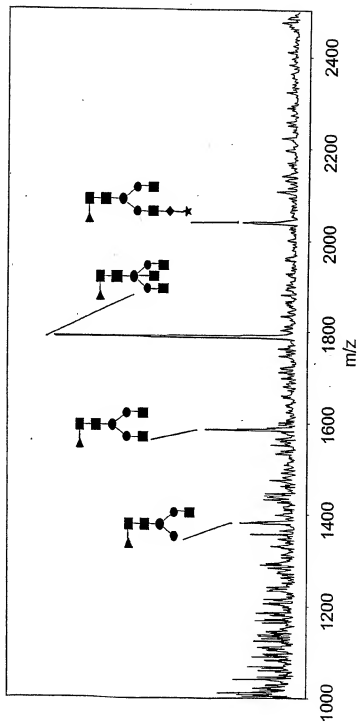


FIG. 111A

391/498

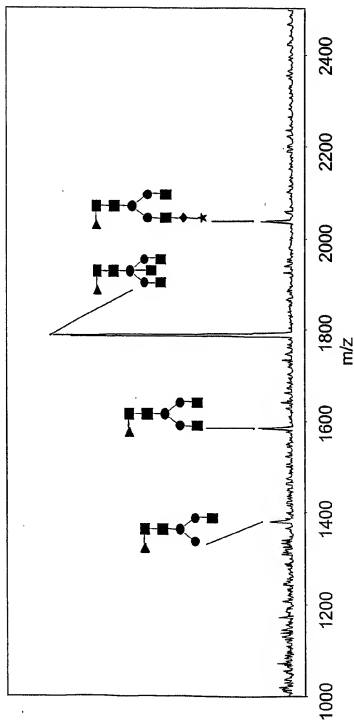


FIG. 111B

392/498

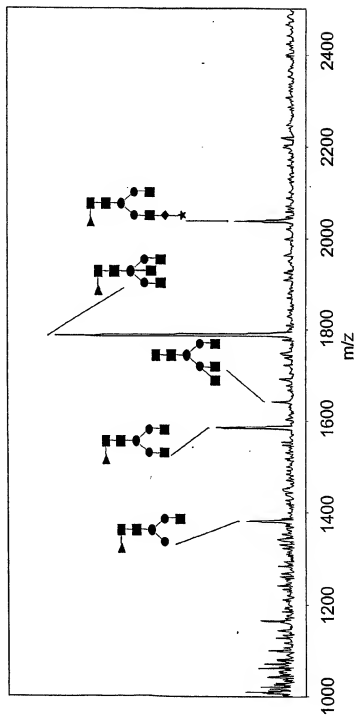


FIG. 111C

393/498

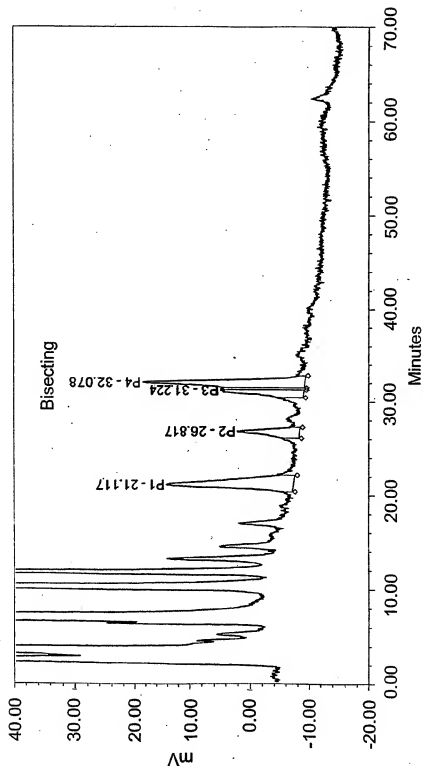


FIG. 112A

394/498

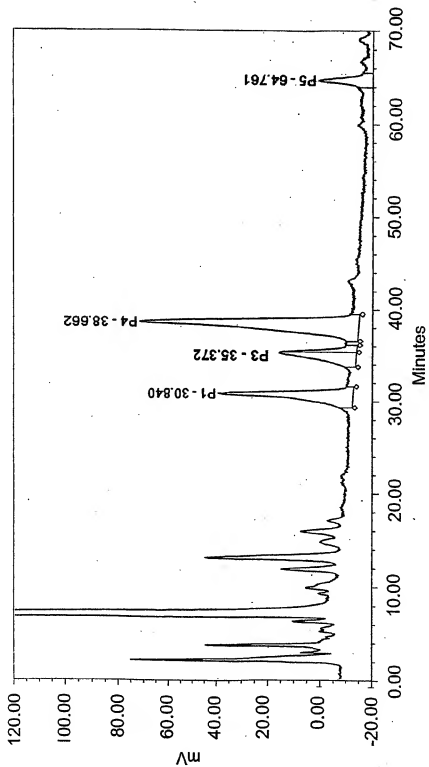


FIG. 112B

395/498

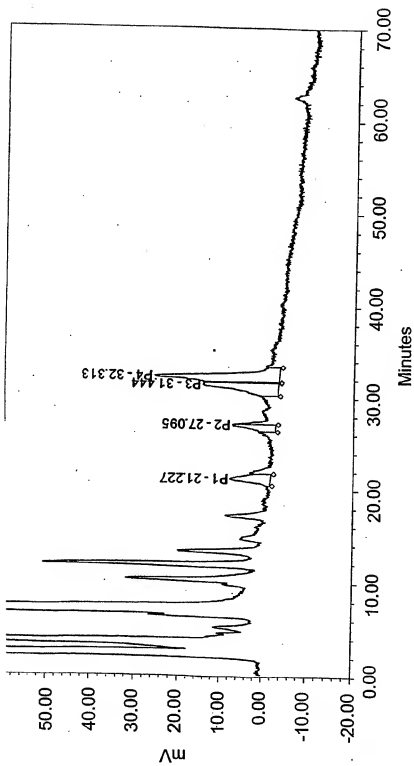


FIG. 112C

396/498

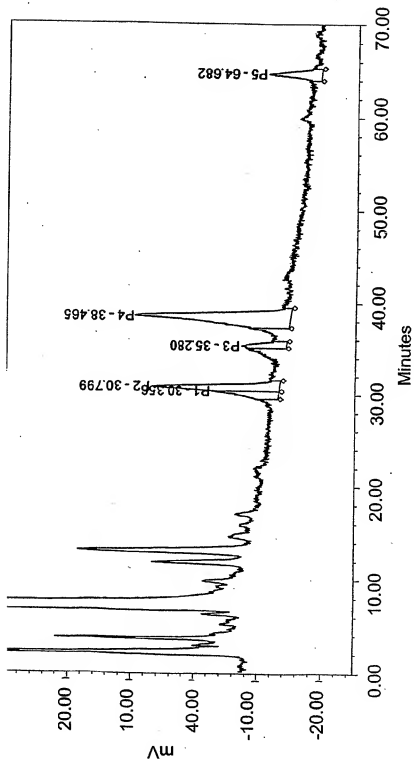


FIG. 112D

397/498

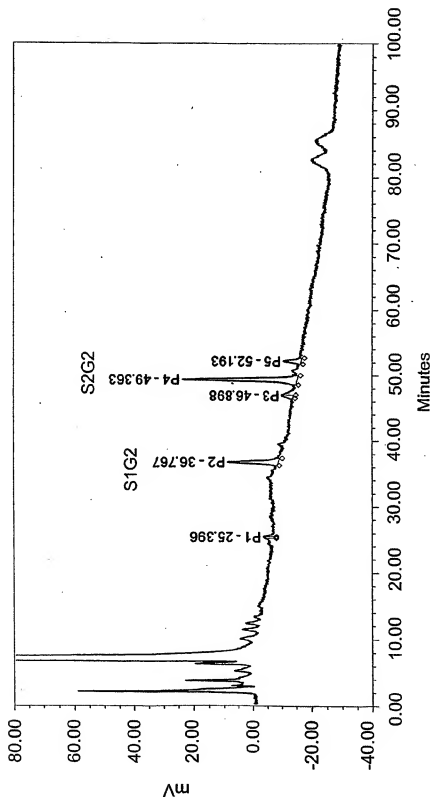


FIG. 113A

398/498

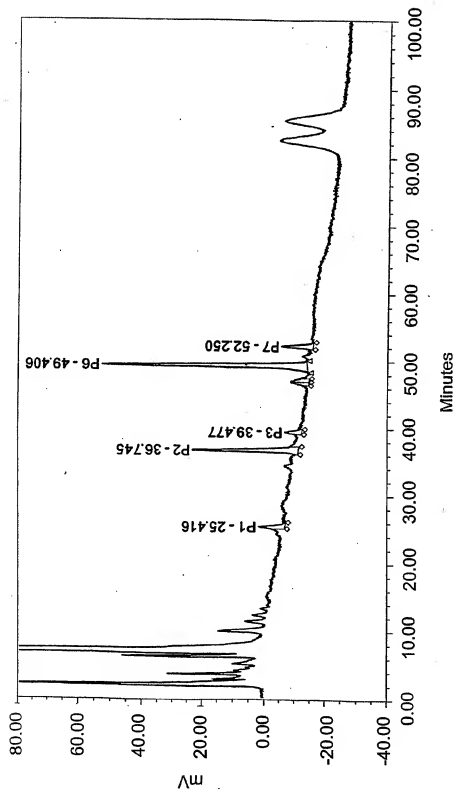


FIG. 113B

399/498

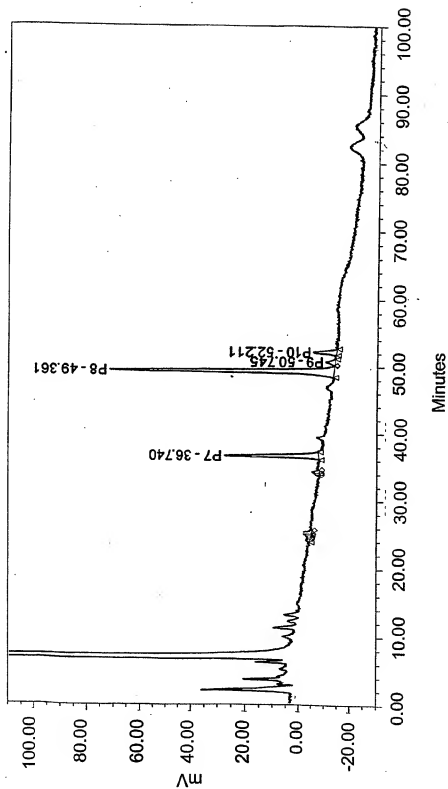


FIG. 113C

400/498

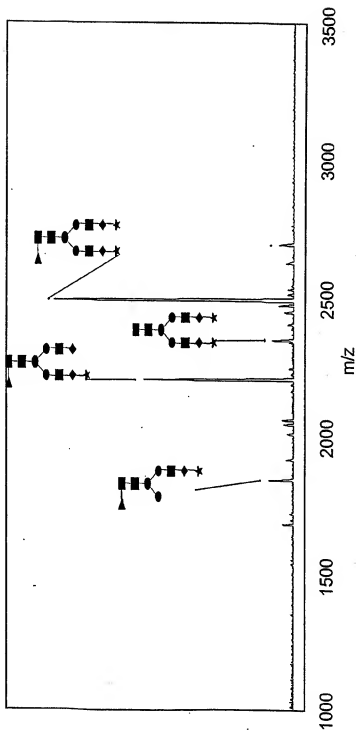


FIG. 114A

401/498

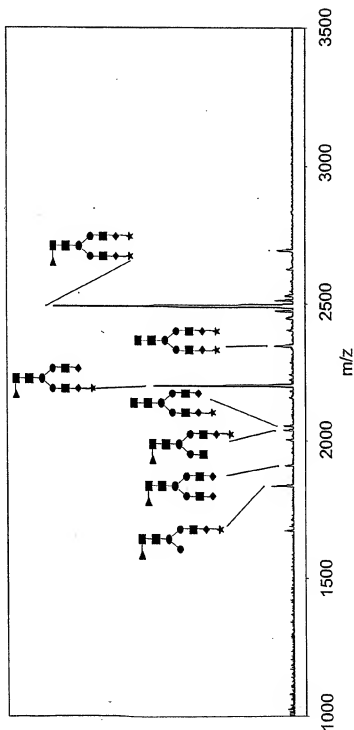


FIG. 114B

402/498

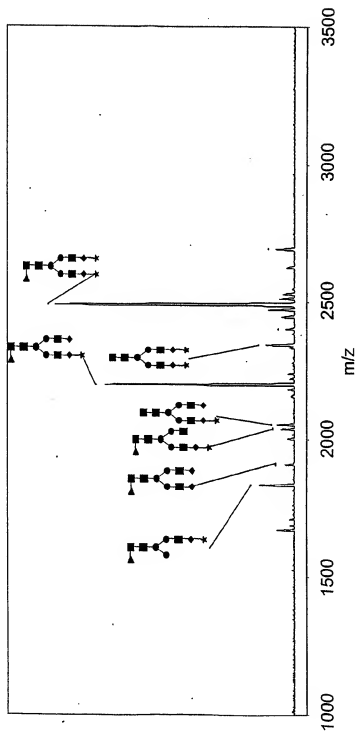


FIG. 114C

403/498

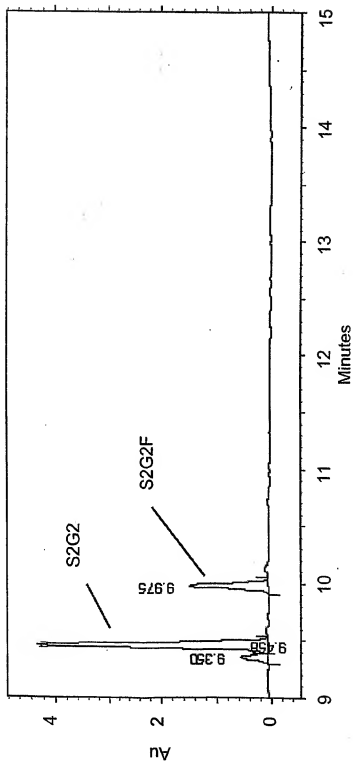


FIG. 115A

404/498

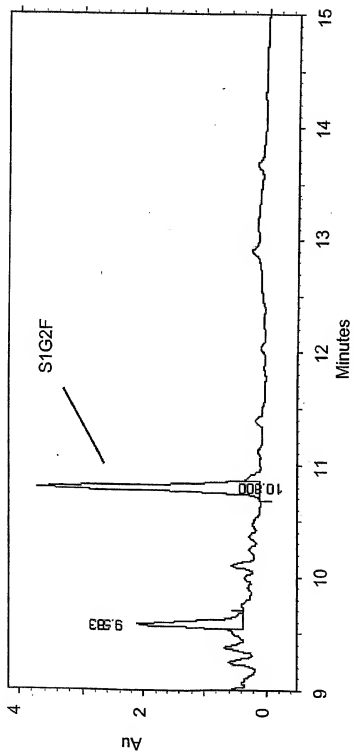


FIG. 115B

405/498

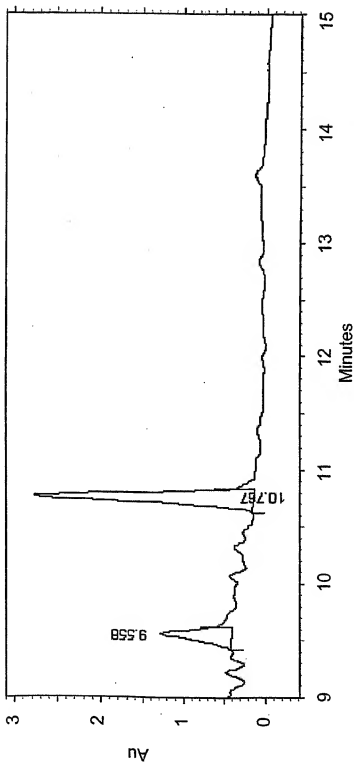


FIG. 115C

406/498

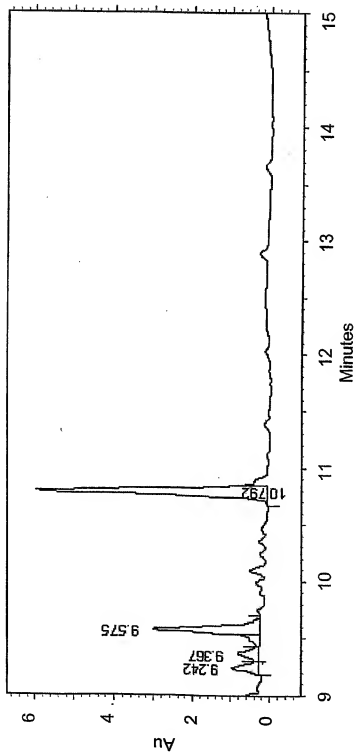


FIG. 115D

407/498

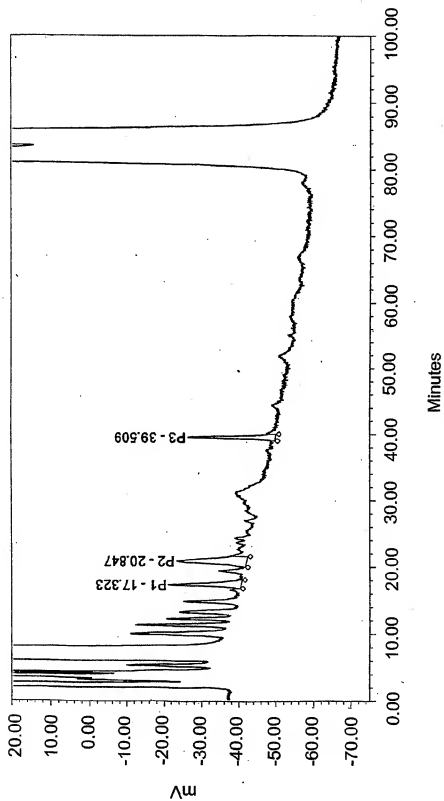


FIG. 116A

408/498

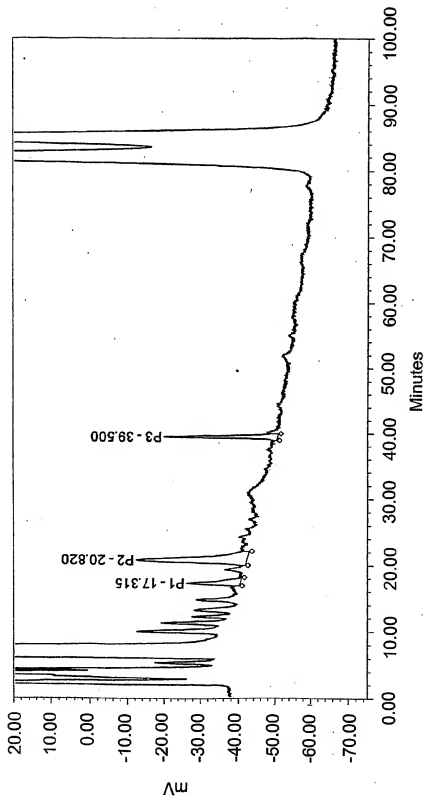


FIG. 116B

409/498

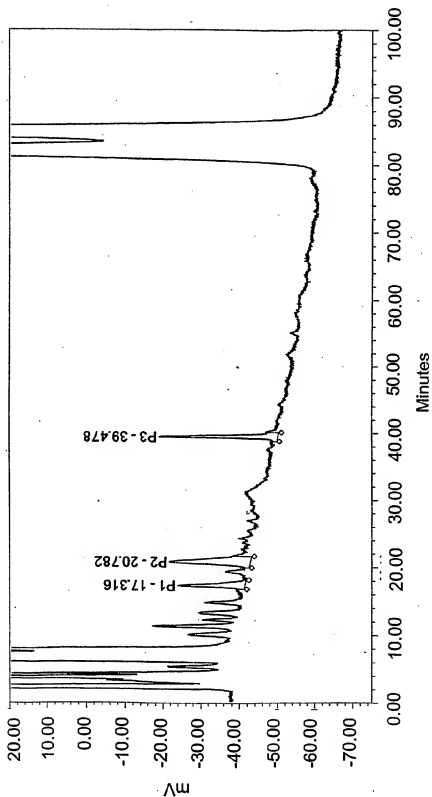


FIG. 116C

410/498

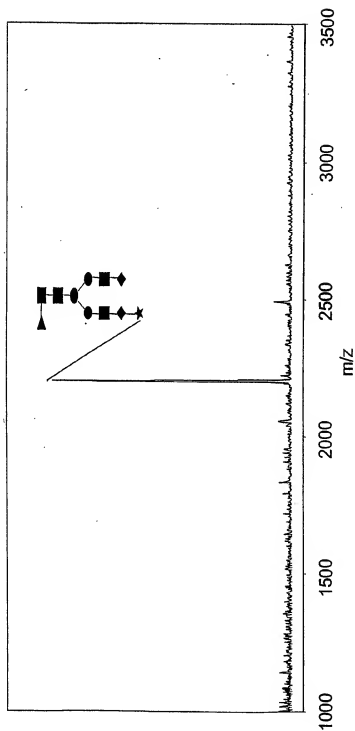


FIG. 117A

411/498

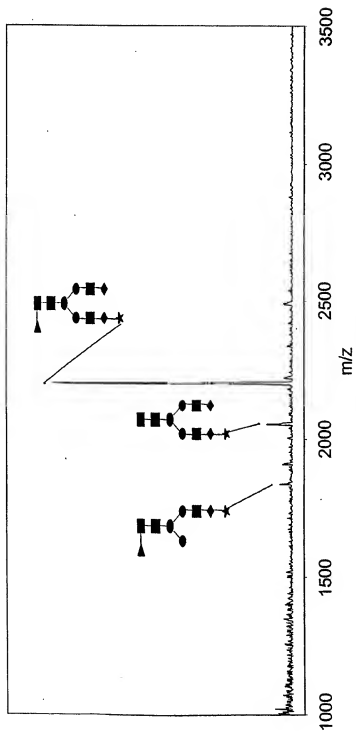


FIG. 117B

412/498

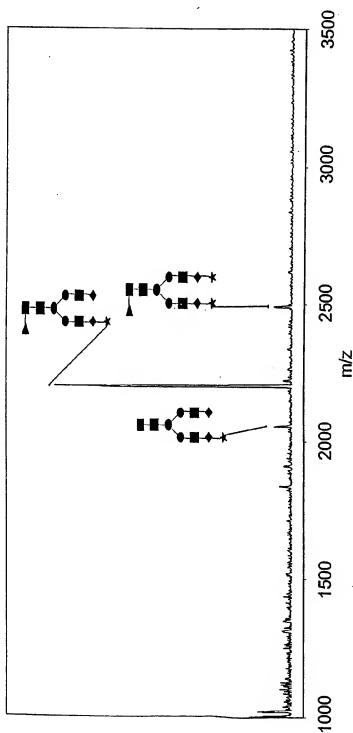


FIG. 117C

413/498

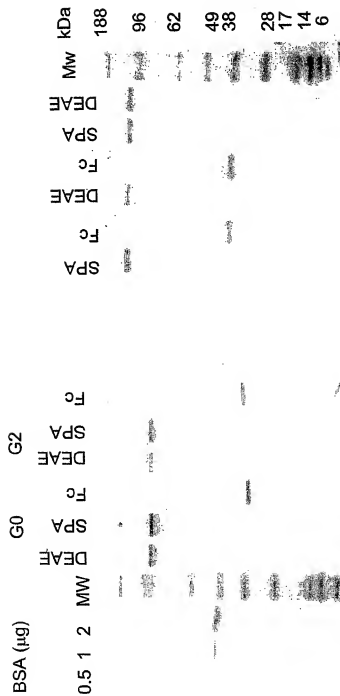


FIG. 118B

FIG. 118A

414/498

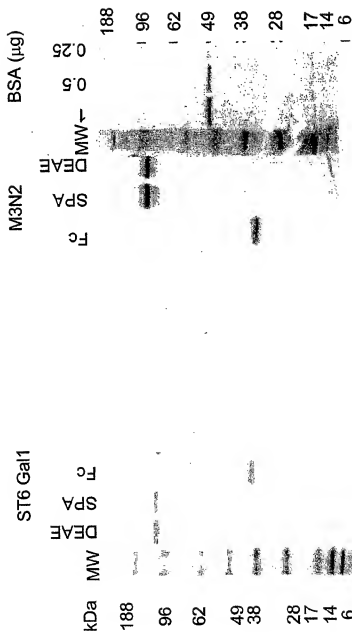


FIG. 118D

FIG. 118C

415/498

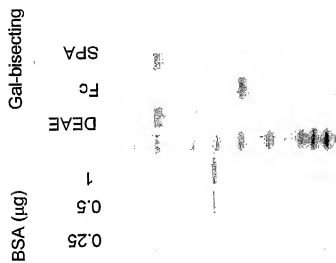


FIG. 118E

416/498

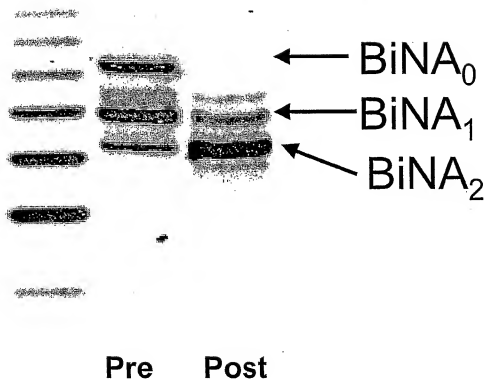


FIG. 119

417/498

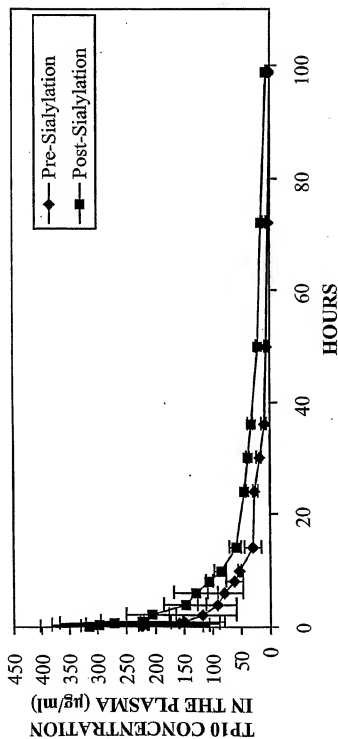


FIG. 120

418/498

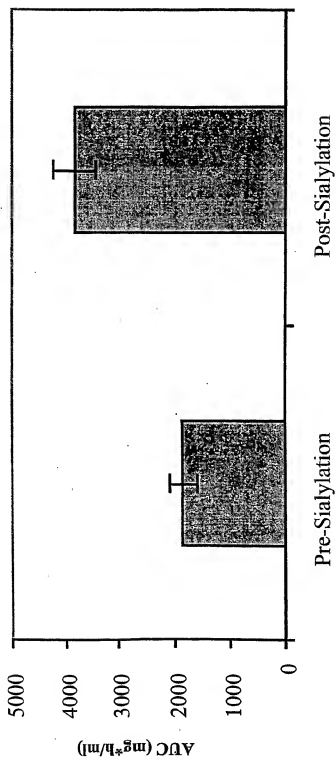


FIG. 121

419/498

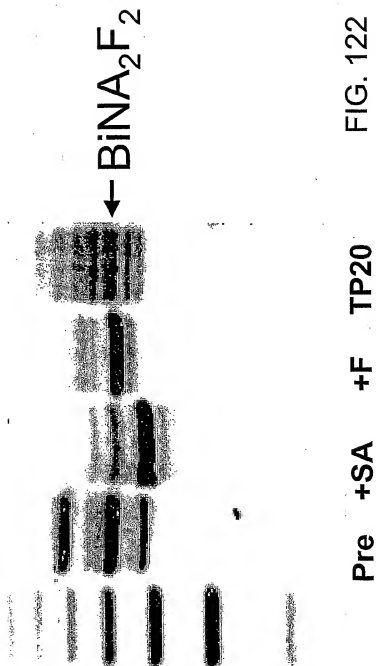


FIG. 122

420/498

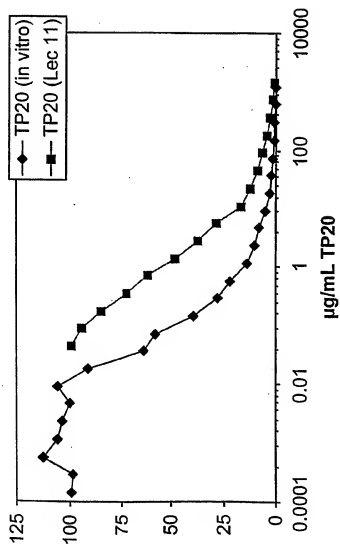


FIG. 123

421/498

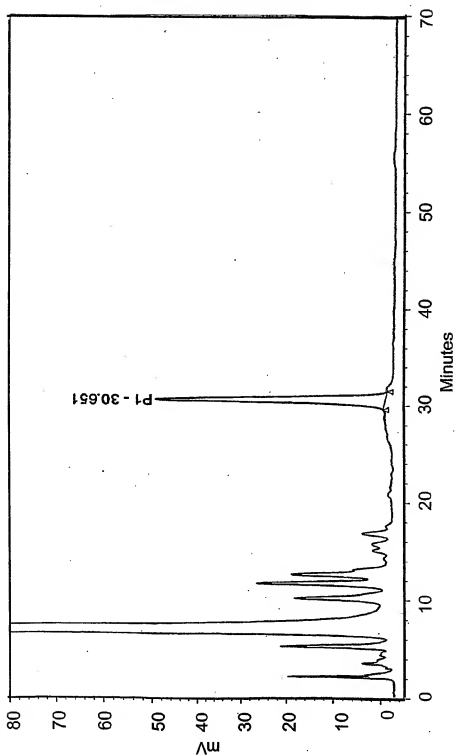


FIG. 124

422/498

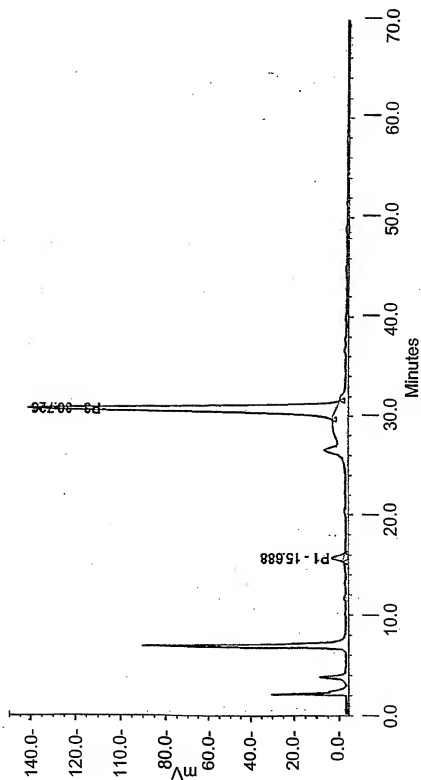


FIG. 125A

423/498

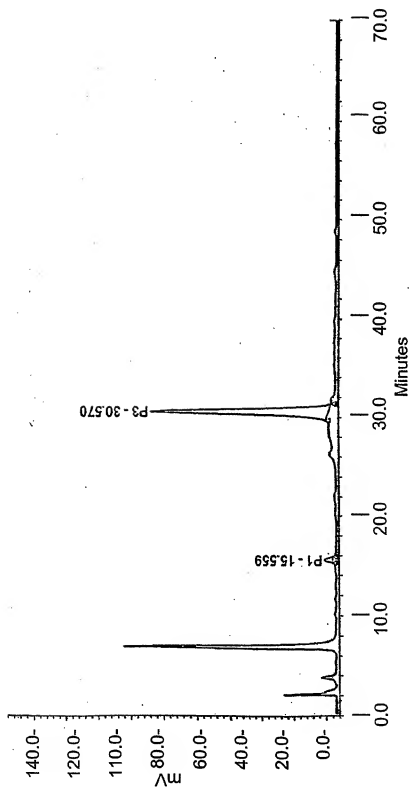


FIG. 125B

424/498

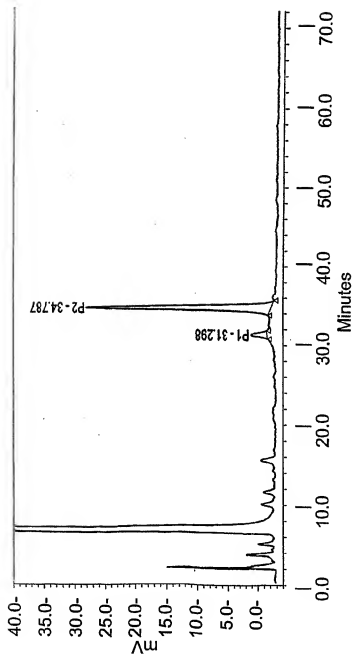


FIG. 126

425/498

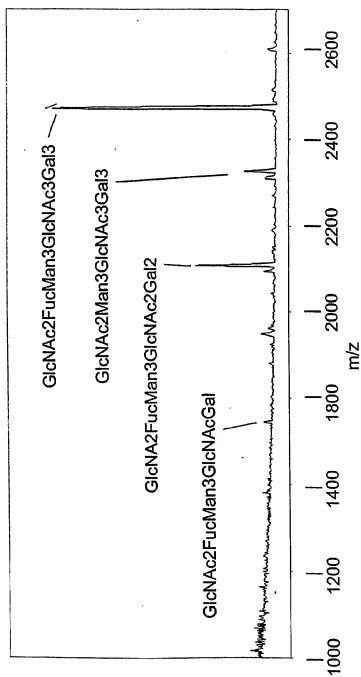


FIG. 127

426/498

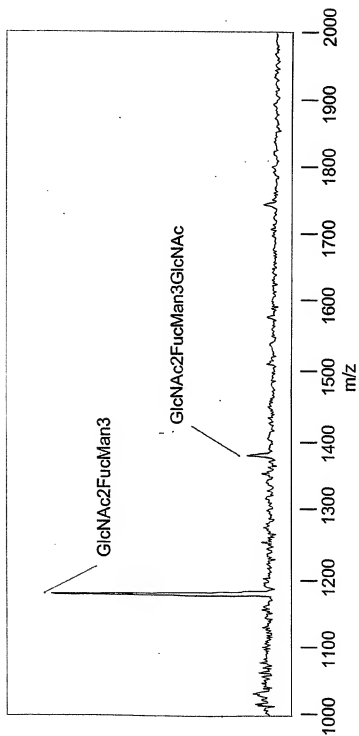


FIG. 128

427/498

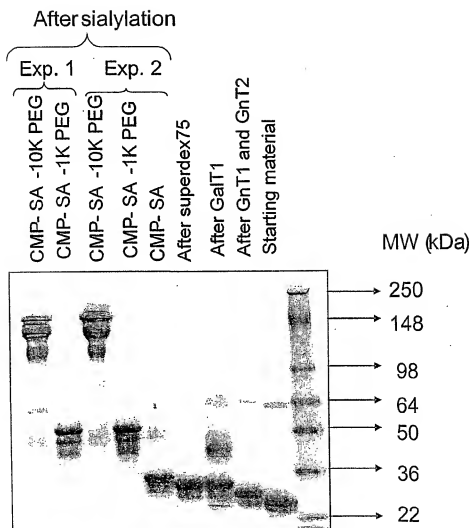


FIG. 129

428/498

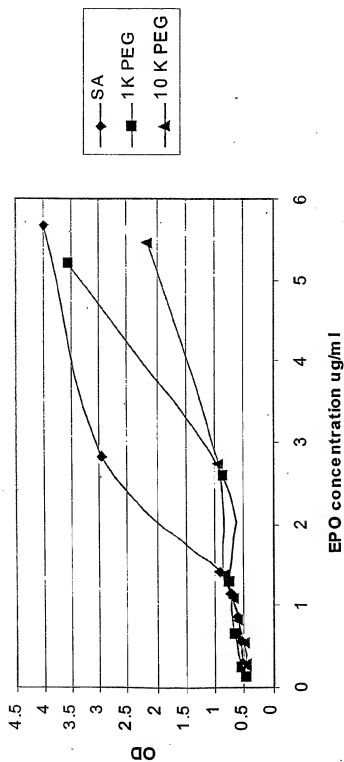
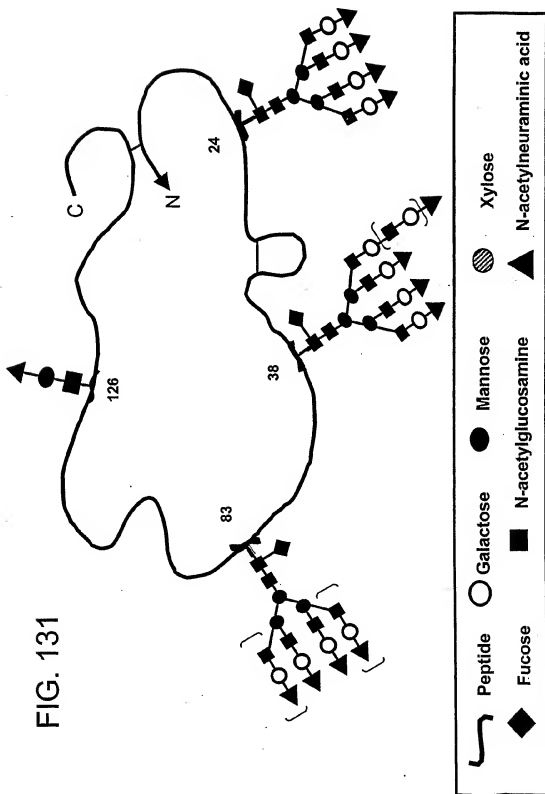


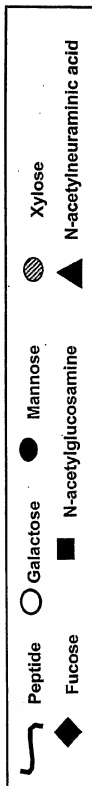
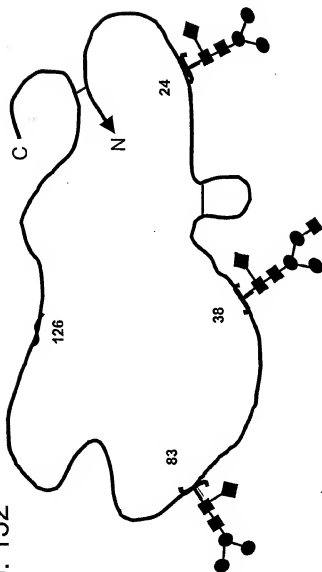
FIG. 130

429/498



430/498

FIG. 132



431/498

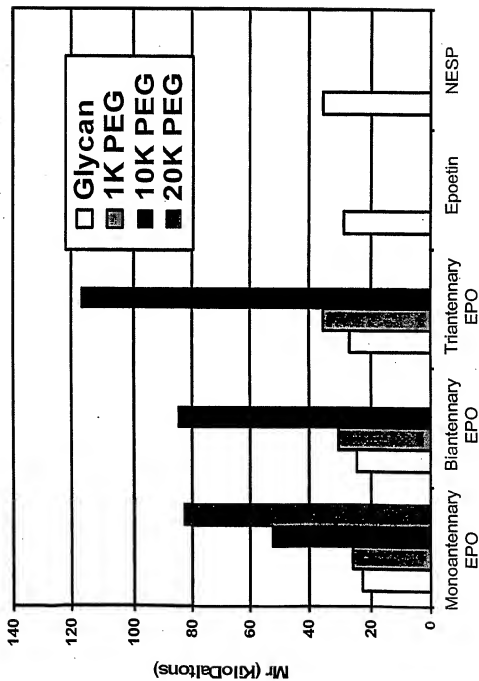
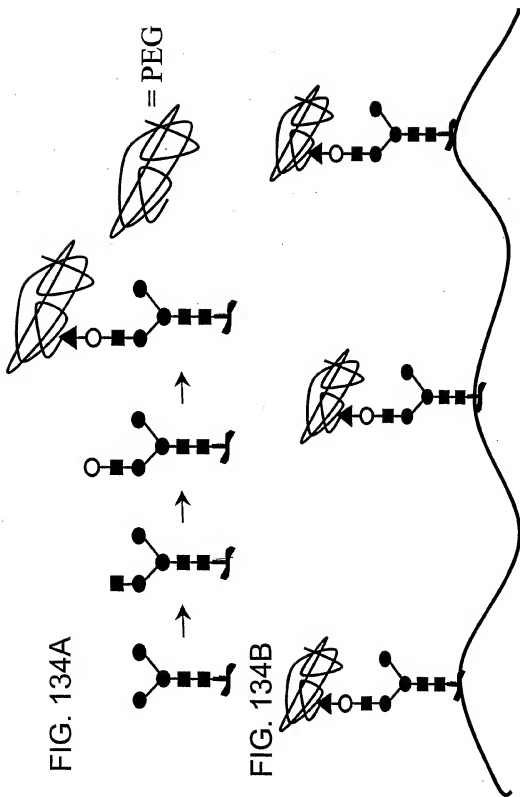


FIG. 133

432/498



433/498

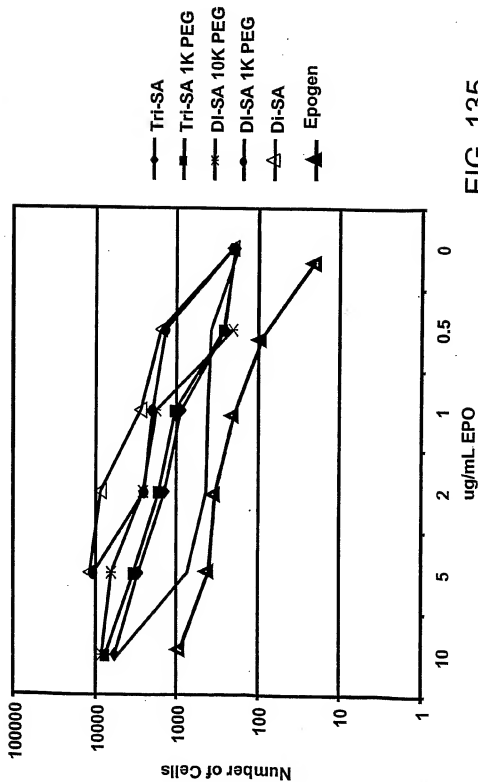


FIG. 135

434/498

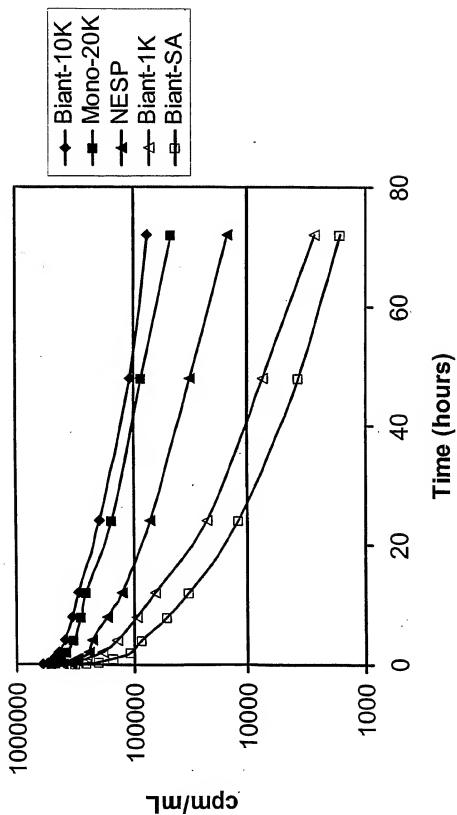


FIG. 136

435/498

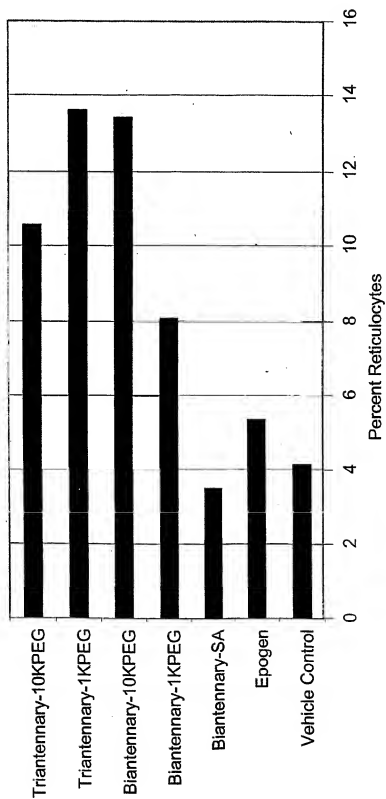


FIG. 137

436/498

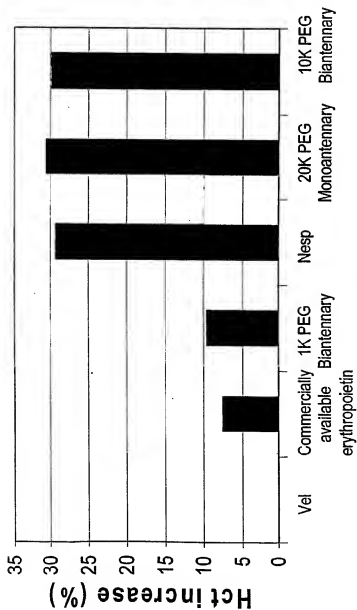


FIG. 138

437/498

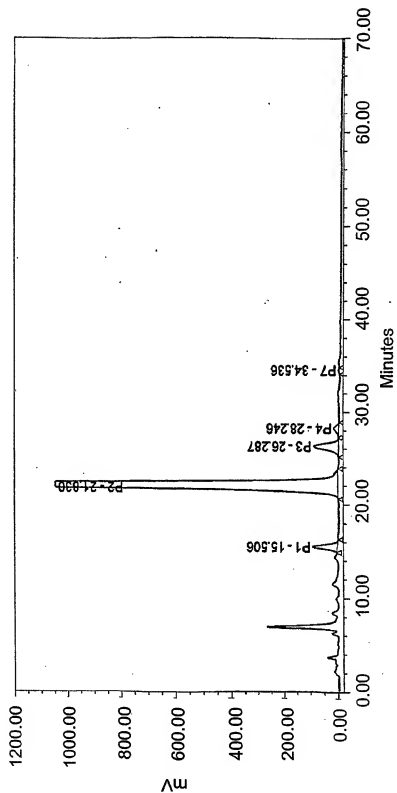


FIG. 139A

438/498

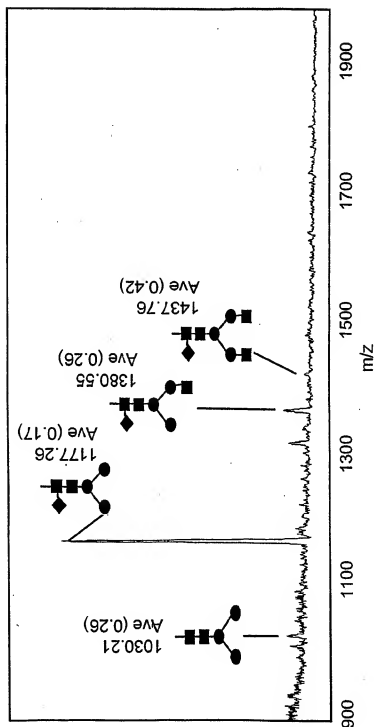


FIG. 139B

439/498

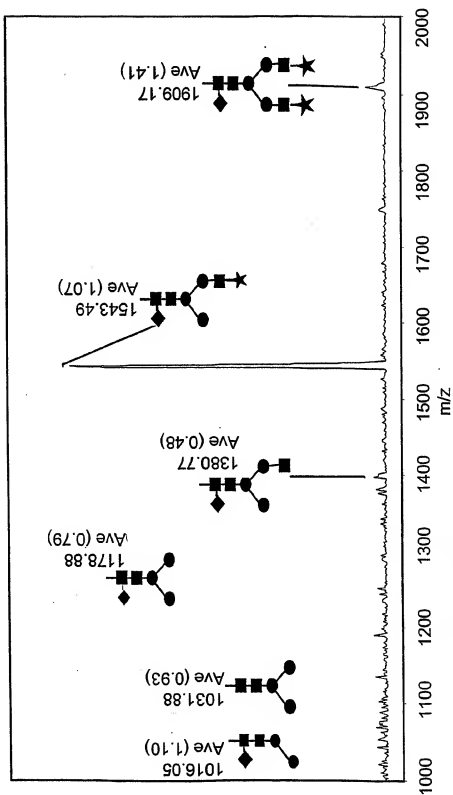


FIG. 140

440/498

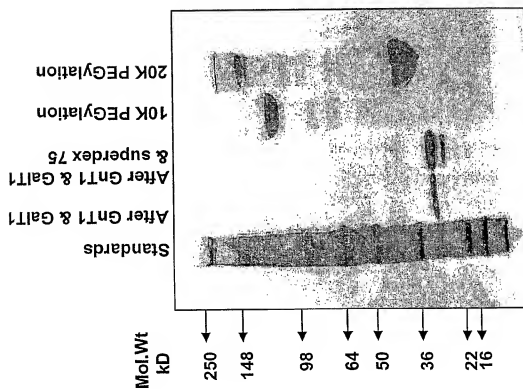


FIG. 141

441/498

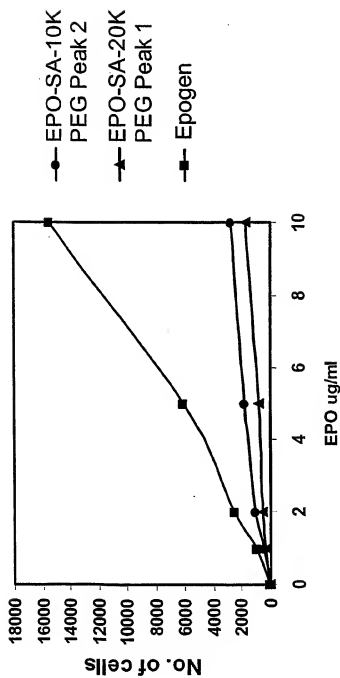


FIG. 142

442/498

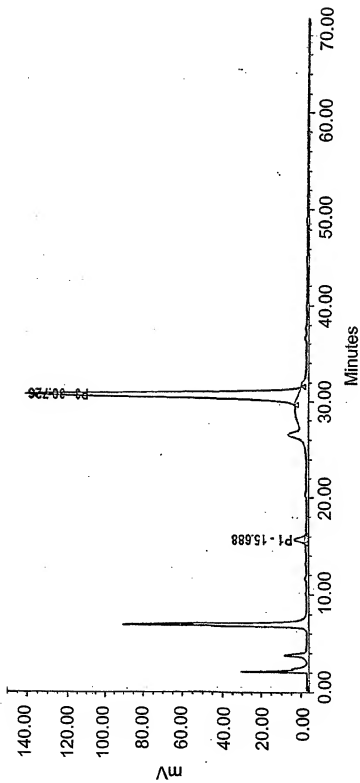


FIG. 143A

443/498

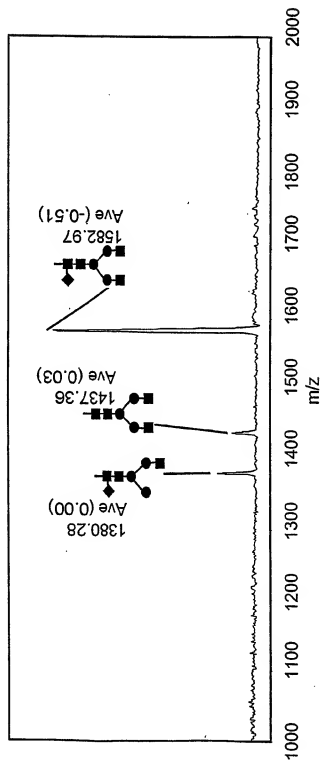


FIG. 143B

444/498

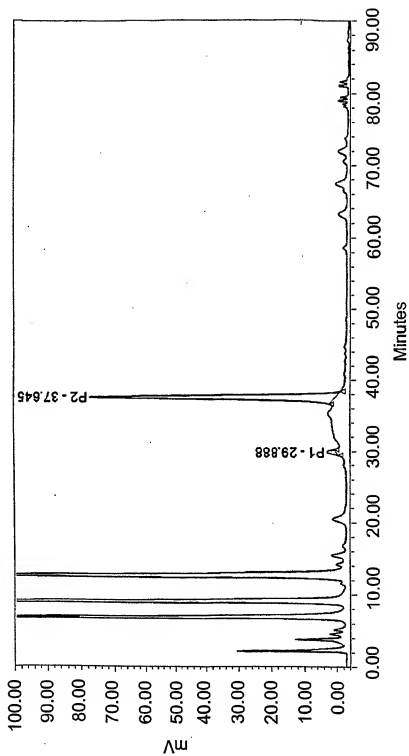


FIG. 144A

445/498

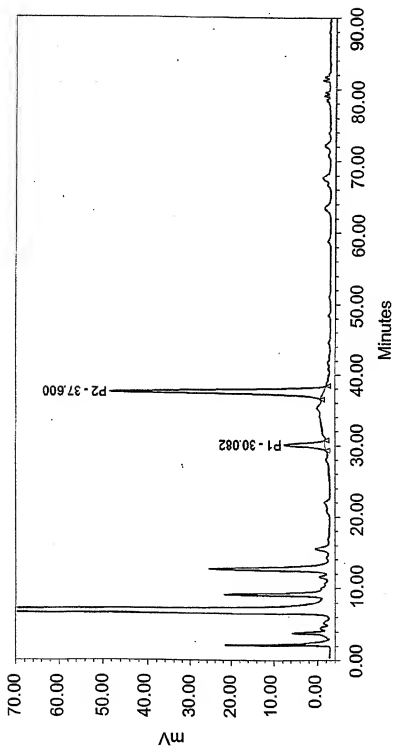


FIG. 144B

446/498

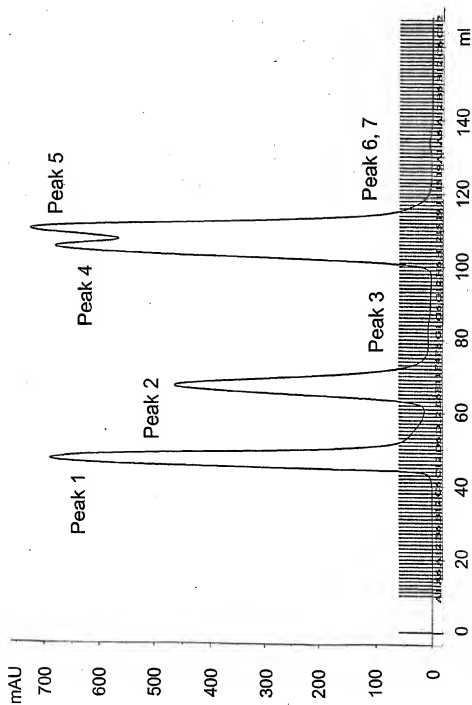


FIG. 145

447/498

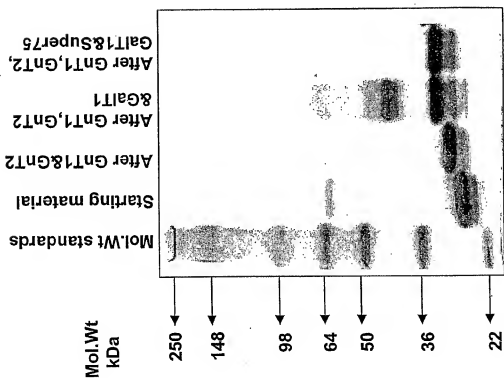


FIG. 146

448/498

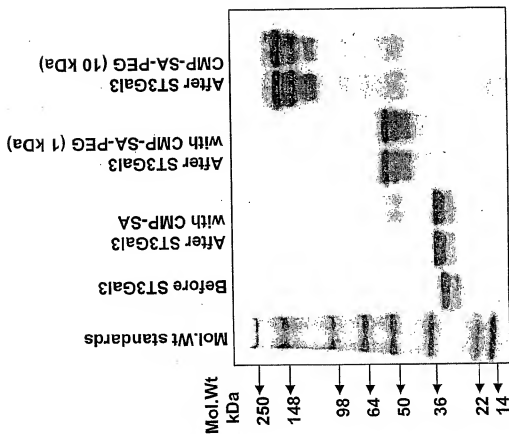


FIG. 147

449/498

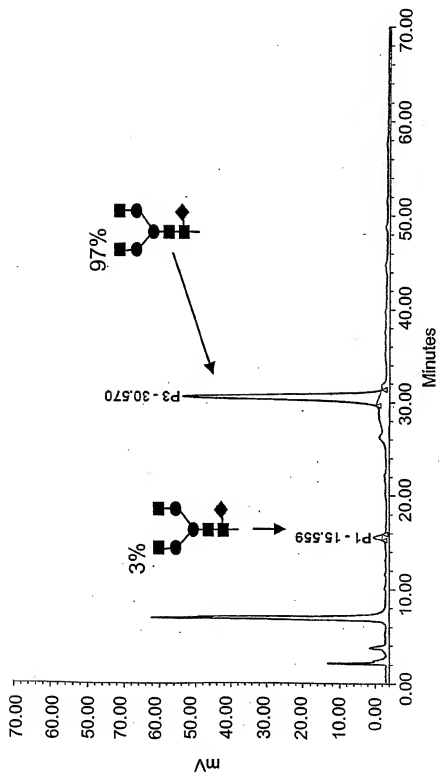


FIG. 148

450/498

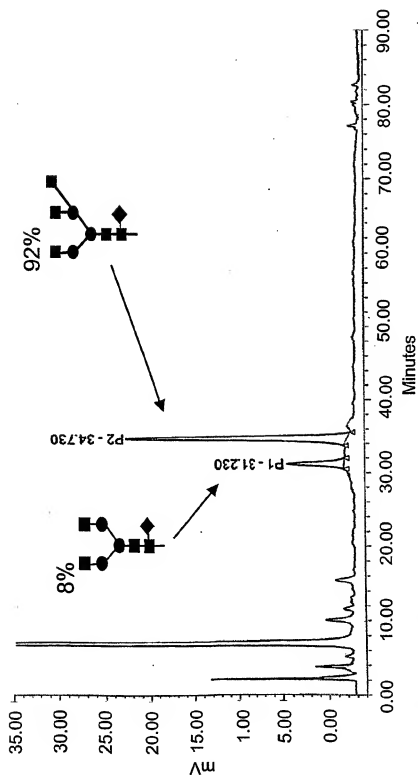


FIG. 149

451/498

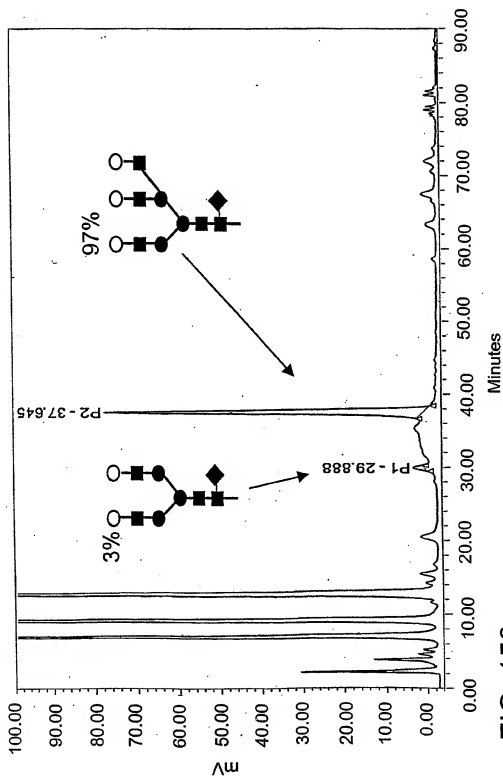


FIG. 150

452/498

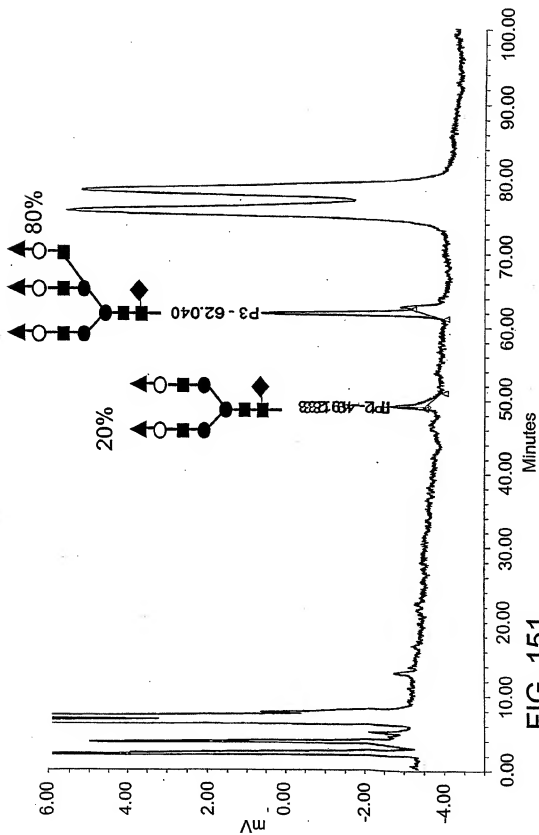


FIG. 151

453/498

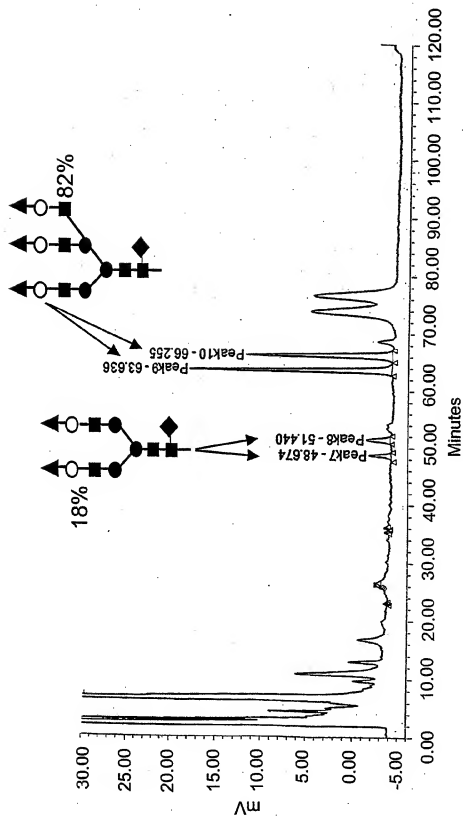


FIG. 152

454/498

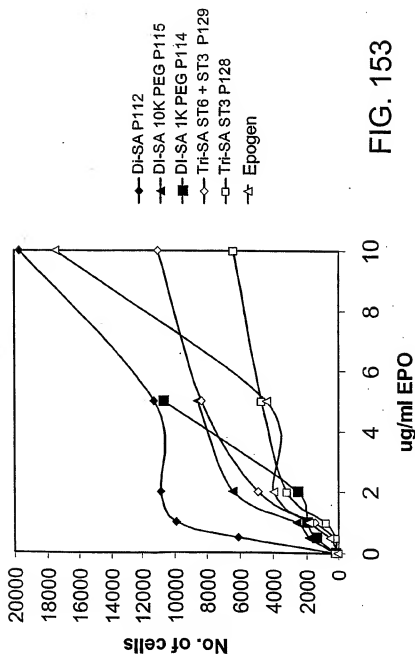


FIG. 153

455/498

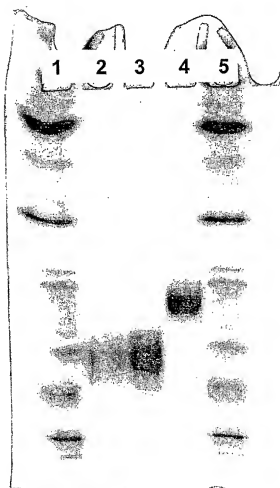


FIG. 154

456/498

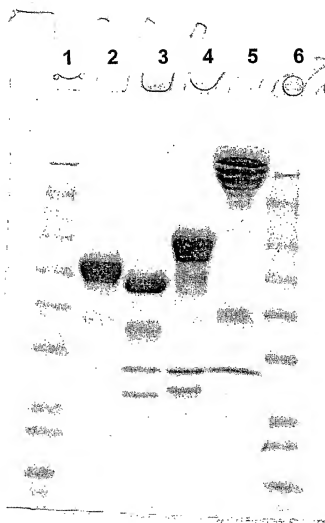


FIG. 155

457/498

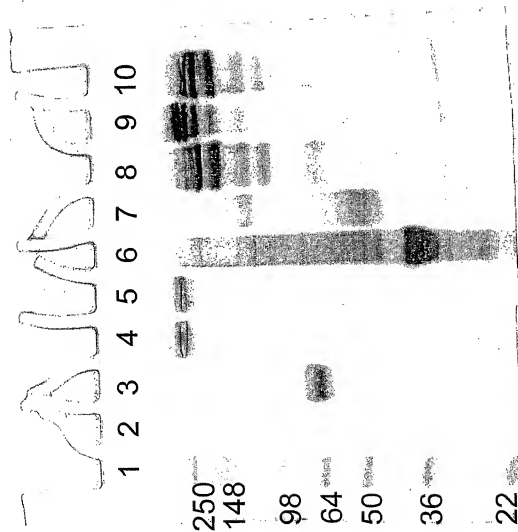


FIG. 156

458/498

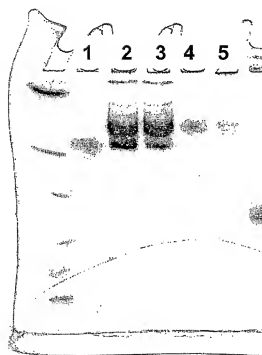


FIG. 157

459/498

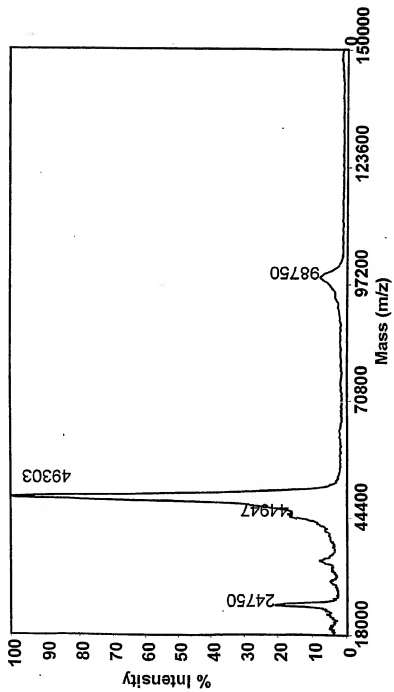


FIG. 158

460/498

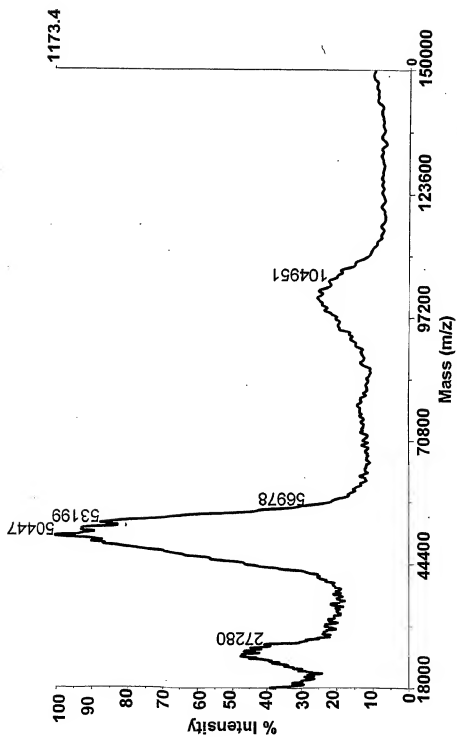


FIG. 159

461/498

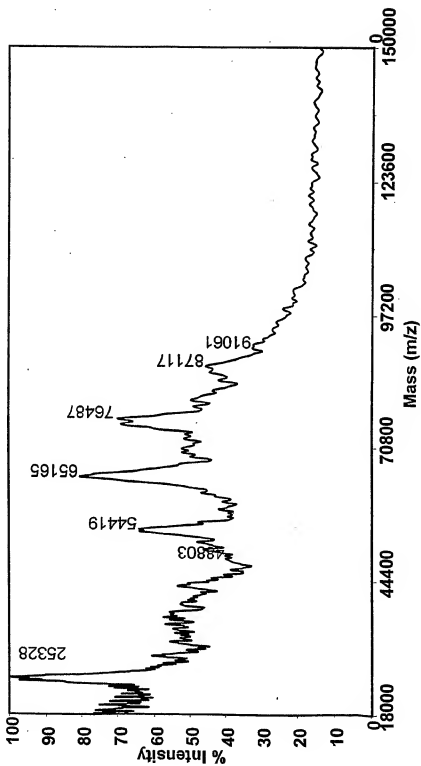


FIG. 160

462/498

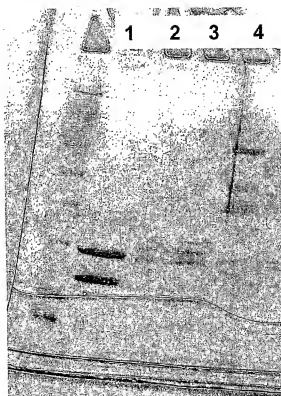


FIG. 161

463/498

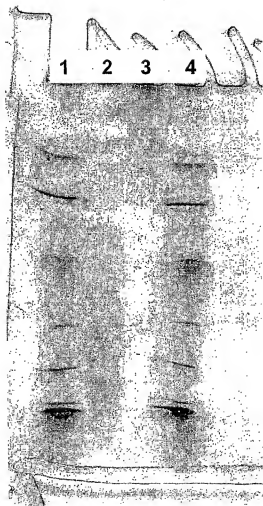


FIG. 162

464/498

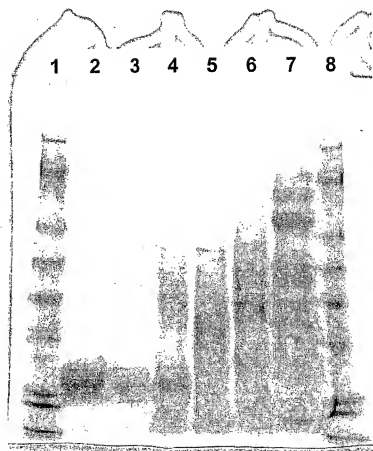


FIG. 163

465/498



FIG. 164

466/498



FIG. 165

467/498

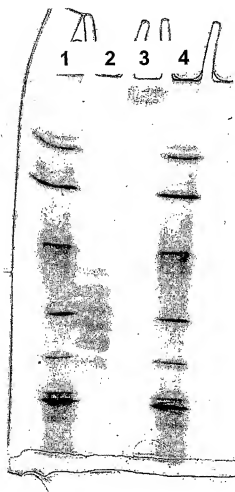


FIG. 166

468/498

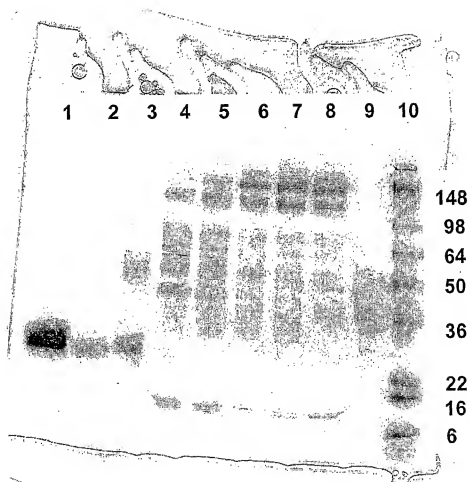


FIG. 167

469/498

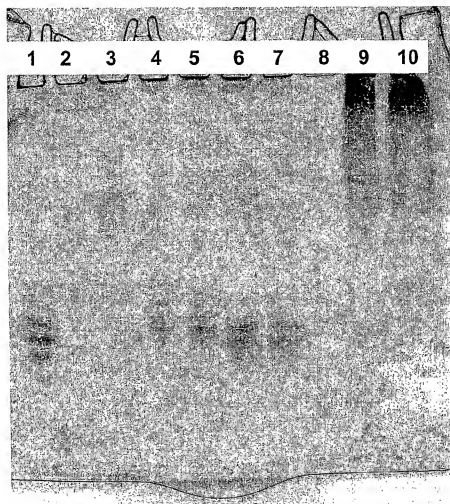
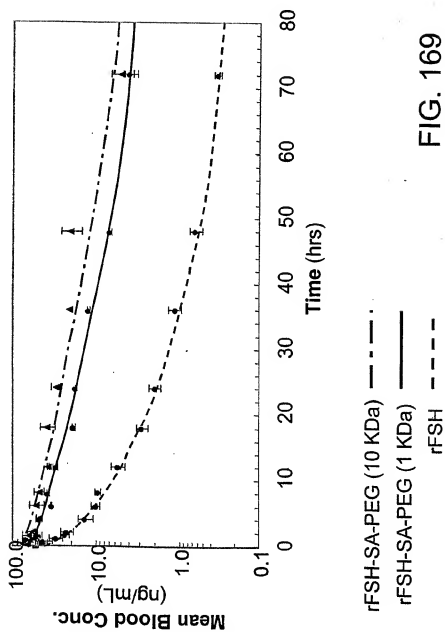


FIG. 168

470/498



471/498

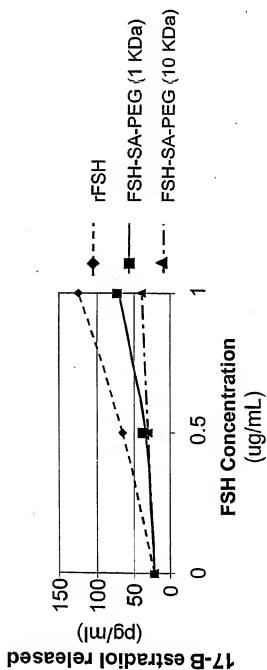


FIG. 170

472/498

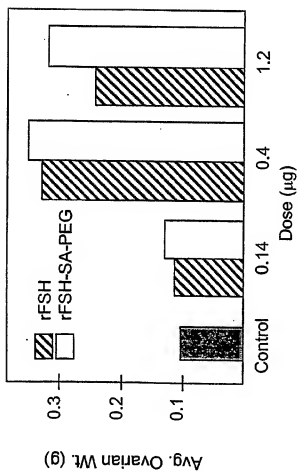


FIG. 171

473/498

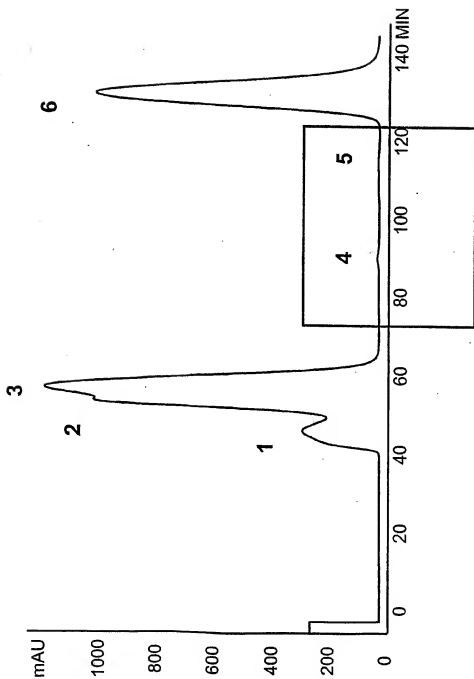


FIG. 172A

474/498

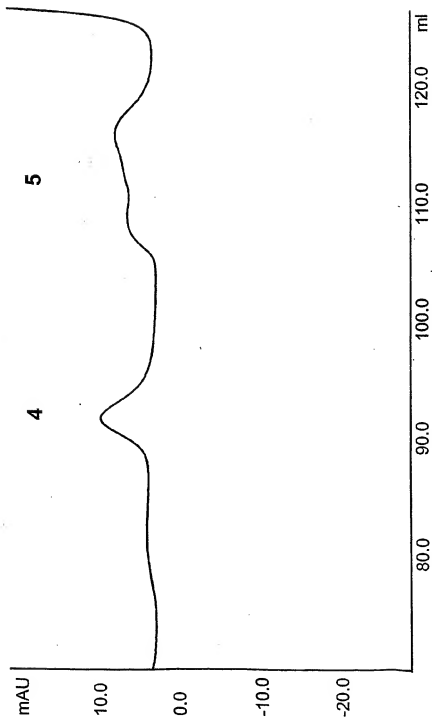


FIG. 172B

475/498

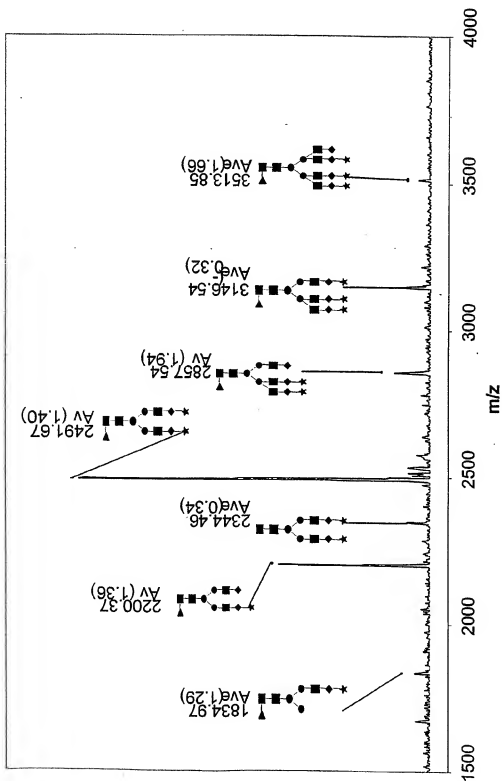


FIG. 173A

476/498

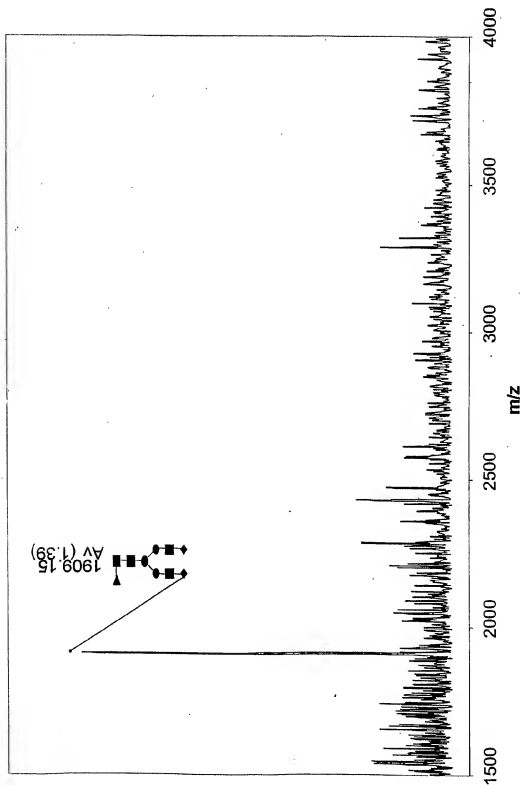


FIG. 173B

477/498

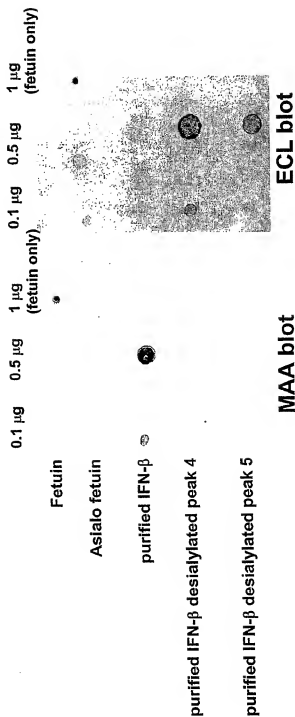


FIG. 174

478/498

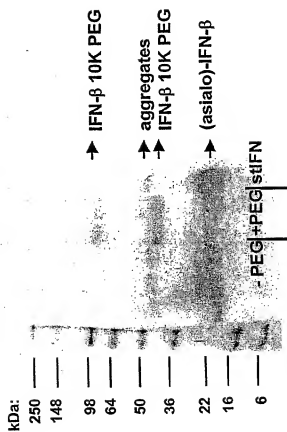
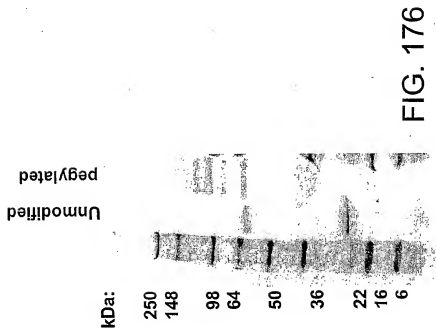


FIG. 175

479/498



480/498

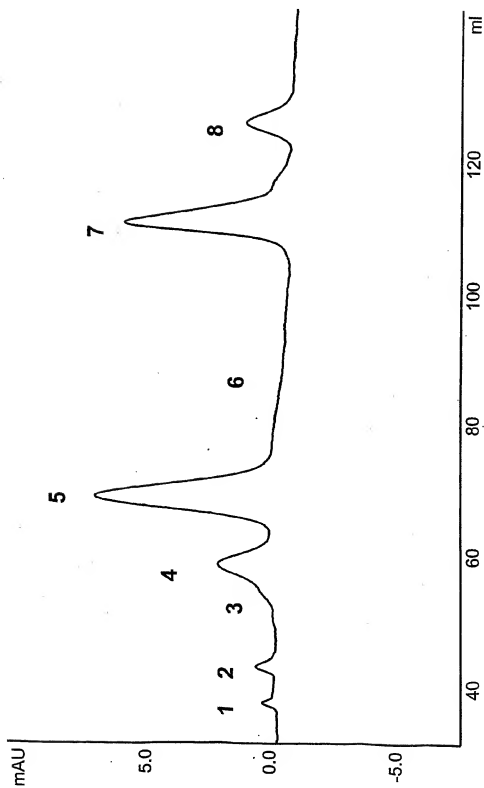


FIG. 177

481/498

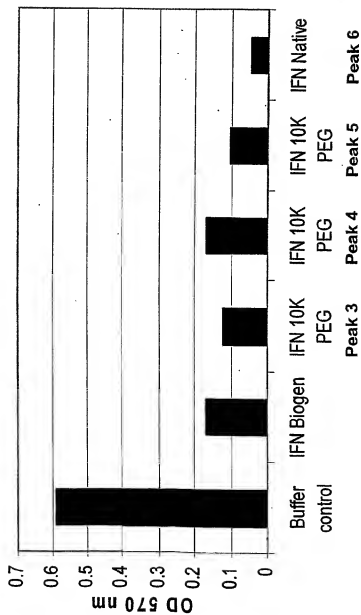


FIG. 178

482/498

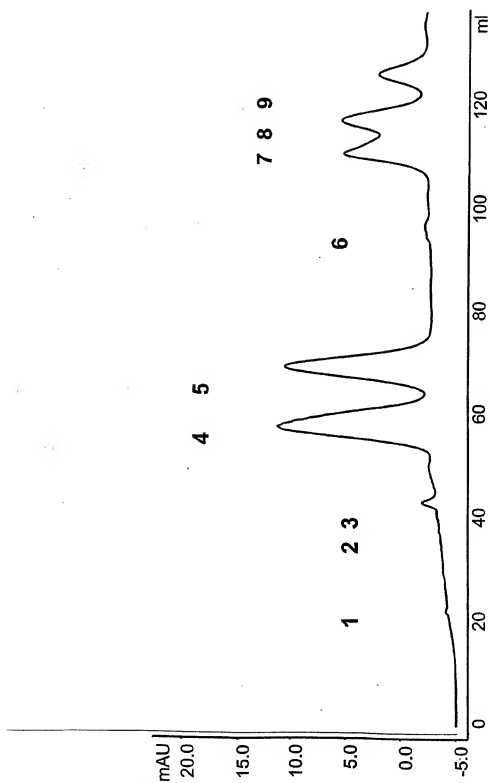


FIG. 179

483/498

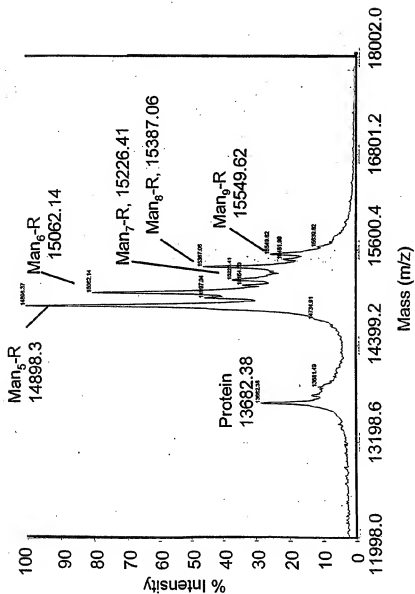


FIG. 180A

484/498

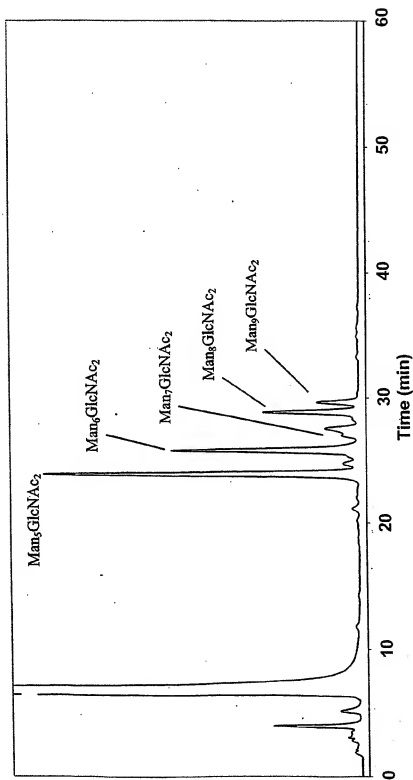


FIG. 180B

486/498

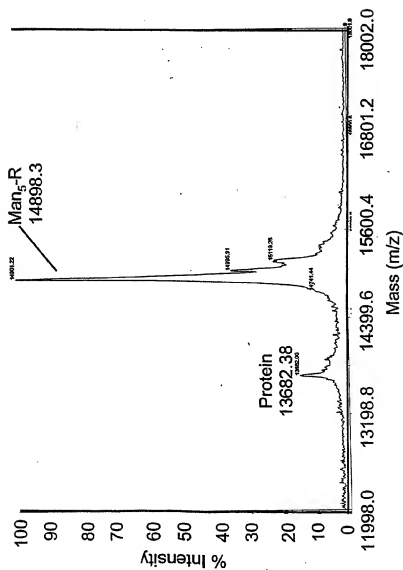


FIG. 182A

487/498

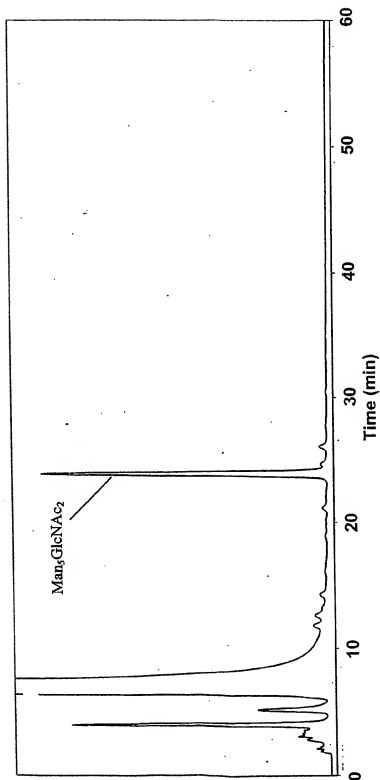


FIG. 182B

490/498

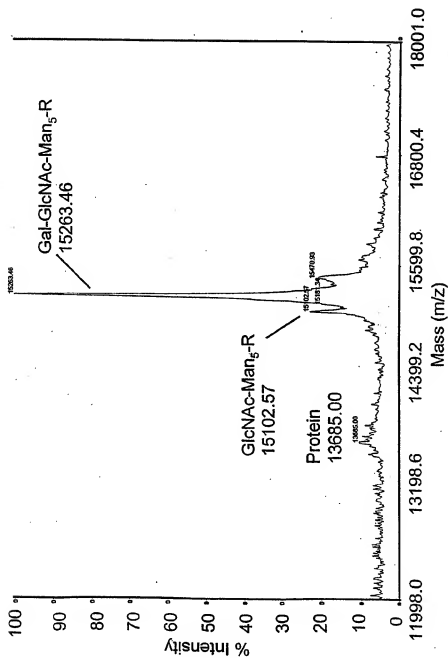


FIG. 185

492/498

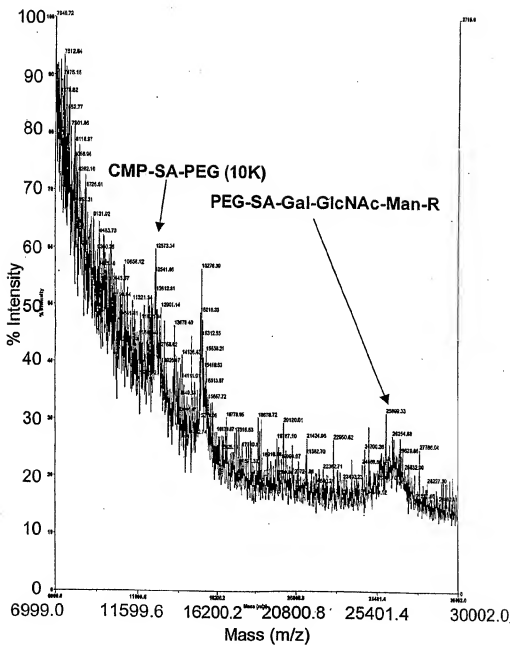
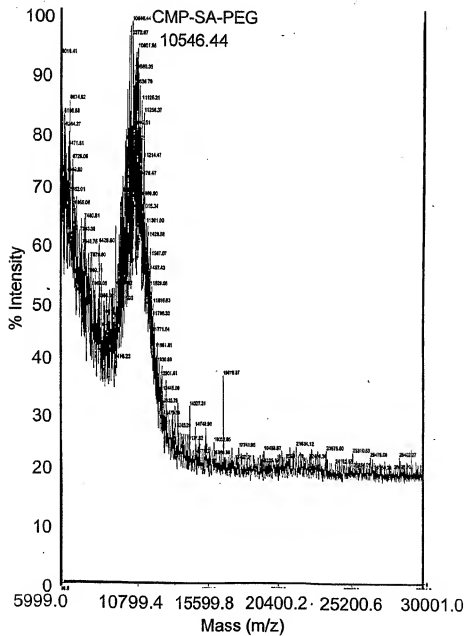


FIG. 187A

493/498



495/498

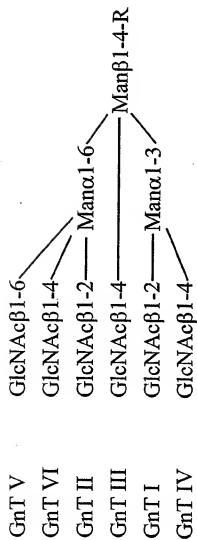


FIG. 189

496/498

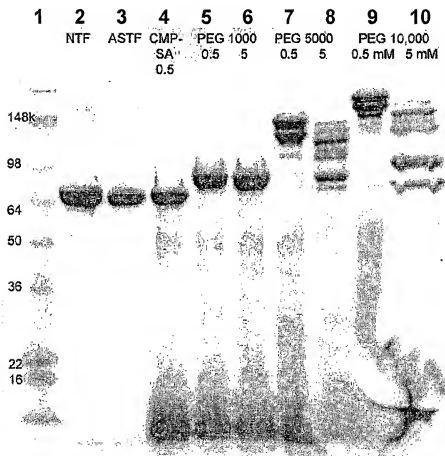


FIG. 190

497/498

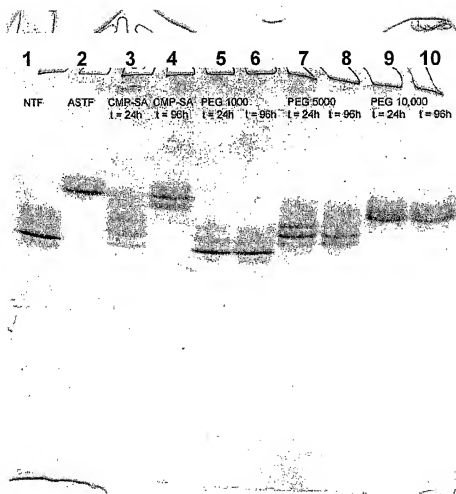
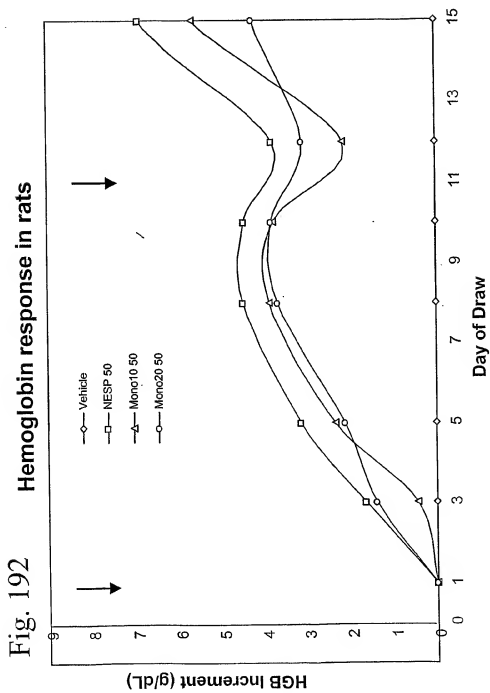


FIG. 191

498/498



SEQUENCE LISTING

<110> Neose Technologies, Inc.
 DeFrees, Shawn
 Zopf, David
 Bayer, Robert
 Hakes, David
 Chen, Xi
 Bowe, Caryne

<120> ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF
 ERYTHROPOIETIN

<130> 040853-01-5083WO

<150> PCT/US02/32263
 <151> 2002-10-09

<150> US 10/287,994
 <151> 2002-11-5

<150> US 10/360,770
 <151> 2003-01-06

<150> US 10/369,779
 <151> 2003-03-17

<150> US 10/410,945
 <151> 2003-04-09

<160> 75

<170> PatentIn version 3.2

<210> 1
 <211> 525
 <212> DNA
 <213> Homo sapiens

<400> 1
 acccccctgg gccctgccag ctccctgcc cagagcttcc tgctcaagtg cttagagcaa 60
 gtgaggaaga tccagggcga tggcgcagcg ctccaggaga agctgtgtgc caccacaag 120
 ctgtgccacc ccgaggagct ggtgctgctc ggacactctc tgggcatccc ctgggctccc 180
 ctgagcagct gccccagcca ggccctgcag ctggcaggct gcttgagcca actccataga 240
 ggccctttcc tetaccaggg gctcctgcag gccctggaag ggatctcccc cgagtgggt 300
 cccaccttgg acacactgca gctggacgtc gccgactttg ccaccacat ctggcagcag 360
 atggaagaac tgggaatggc ccctgccctg cagccacccc aggtgtgcat gccggccttc 420
 gcctctgctt tccagcgcg gccaggagggt gtcctgggtg cctcccatct gcagagcttc 480
 ctggagggtg cgtaccgcgt tctacgccac cttgcccagc cctga 525

<210> 2
 <211> 174
 <212> PRT

<213> Homo sapiens

<400> 2

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
 1 5 10 15

Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Leu Val
 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 165 170

<210> 3

<211> 1733

<212> DNA

<213> Homo sapiens

<400> 3

gagcctctta tgtaccacca aaaatctatt ttcaaaaaag ttgctctaag aatatagtta 60

tcaagttaag taaaatgtca atagcctttt aatttaattt ttaattgttt tatcattcctt 120

tgcaataata aaacattaac ttatatacttt ttaattttaat gtatagaata gagatataca 180

taggatattgt aaatagatac acagtgtata tgtgattaaa atataatggg agattcaatc 240

agaaaaaagt ttctaaaaag gctctggggt aaaagaggaa ggaacaata atgaaaaaaa 300

tgtggtgaga aaacacagctg aaaccccatg taaagagtgt ataaagaaag caaaaagaga 360

agtagaaaagt aacacagggg catttggaag atgtaaacga gtatgttccc tatttaaggc 420

taggcacaaa gcaaggtctt cagagaacct ggagcctaag gtttaggctc acccatttca 480

accagtctag cagcatctgc aacatctaca atggccttga cctttgcttt actggtggcc 540

ctcctggtgc tcagctgcaa gtcaagctgc tctgtgggct gtgatctgcc tcaaaaccac 600


```

agcctgggta gcaggaggac cttgatgctc ctggcacaga tggaggagaat ctctcttttc 660
tctctgttga aggacagaca tgactttgga tttccccagg aggagtttgg caaccagttc 720
caaaaggctg aaaccatccc tgtcctccat gagatgatcc agcagatctt caatctcttc 780
agcacaaagg actcatctgc tgcctgggat gagaccctcc tagacaaatt ctacactgaa 840
ctctaccagc agctgaatga cctggaagcc tgtgtgatac aggggggtgg ggtgacagag 900
actccoctga tgaaggagga ctccattctg gctgtgagga aatacttcca aagaatact 960
ctctatctga aagagaagaa atacagccct tgtgcctggg aggttgtcag agcagaaatc 1020
atgagatctt tttctttgtc aacaaacttg caagaaagt taagaagtaa ggaatgaaaa 1080
ctgggtcaac atggaaatga ttttcattga ttctatgcc agctcacctt tttatgatct 1140
gccatttcaa agactcatgt ttctgctatg accatgacac gatttaaatc ttttcaatg 1200
tttttaggag tattaatcaa cattgtatc agctcttaag gcactagtcc cttacagagg 1260
accatgctga ctgatccatt atctatttaa atatttttaa aatattttt atttaactat 1320
ttataaaaca acttattttt gttcatatta tgcattgtgc acctttgcac agtggttaat 1380
gtaataaaat gtgtctcttg tatttggtaa atttattttg tgttgttcac tgaacttttg 1440
ctatggaact ttgtacttg tttattctt aaaatgaaat tccaagccta attgtgcaac 1500
ctgattacag aataactggt acaattcatt tgtccatcaa tattatattc aagatataag 1560
taaaaataaa cttctgttaa accaagttgt atgtgtgact caagataaca ggtggaacct 1620
aacaataata attctgctct cttgtgtatt tgatttttgt atgaaaaaaa ctaaaaatgg 1680
taatcatact taattatcag ttatggtaaa tggatatgaag agaagaagga acg 1733

```

```

<210> 4
<211> 188
<212> FRT
<213> Homo sapiens

```

```

<400> 4
Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
1 5 10 15
Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
20 25 30
Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
35 40 45
Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
50 55 60
Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
65 70 75 80
Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser

```

85										90					95				
Ala	Ala	Trp	Asp	Glu	Thr	Leu	Leu	Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr				
			100						105					110					
Gln	Gln	Leu	Asn	Asp	Leu	Glu	Ala	Cys	Val	Ile	Gln	Gly	Val	Gly	Val				
			115					120					125						
Thr	Glu	Thr	Pro	Leu	Met	Lys	Glu	Asp	Ser	Ile	Leu	Ala	Val	Arg	Lys				
			130				135					140							
Tyr	Phe	Gln	Arg	Ile	Thr	Leu	Tyr	Leu	Lys	Glu	Lys	Lys	Tyr	Ser	Pro				
145					150					155					160				
Cys	Ala	Trp	Glu	Val	Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Leu				
				165					170						175				
Ser	Thr	Asn	Leu	Gln	Glu	Ser	Leu	Arg	Ser	Lys	Glu								
				180					185										

<210> 5
 <211> 757
 <212> DNA
 <213> Homo sapiens

<400> 5
 atgaccaaca agtgctcctt ccaaattgct ctctgttgt gcttctccac tacagctctt 60
 tccatgagct acaacttgct tggattccta caaagaagca gcaattttca gtgtcagaag 120
 ctctgtggc aattgaatgg gaggttgaa tattgctca aggacaggat gaactttgac 180
 atccttgagg agattaagca gctgcagcag ttccagaagg aggaagccgc attgaccatc 240
 tatgagatgc tccagaacat ctttgctatt ttccagacaag attcatctag cactggctgg 300
 aatgagacta ttgttgagaa cctctggct aatgtctatc atcagataaa ccacttgaag 360
 acagtctcgg aagaaaaact ggagaaagaa gattttacca ggggaaaact catgagcagt 420
 ctgcacctga aaagatatta tgggaggatt ctgcattacc tgaaggccaa ggagtacagt 480
 cactgtgctt ggaccatagt cagagtggaa atcctaagga acttttactt cattaacaga 540
 cttacaggtt acctcggaaa ctgaagatct cctagcctgt cctctgggga ctggacaatt 600
 gcttoaagca ttctcaacc agcagatgct gtttaagtga ctgtaggcta atgtactgca 660
 aatgaaagga cactagaaga ttttgaaatt tttattaaat tatgagttat ttttatttat 720
 ttaaatttta ttttggaana taaattattt ttggtgc 757

<210> 6
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
 1 5 10 15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
 20 25 30
 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45
 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60
 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80
 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95
 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125
 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140
 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
 145 150 155 160
 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
 165 170 175
 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 180 185

<210> 7

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 7

atgggtctccc aggcctcag gctcctctgc cttctgcttg ggcttcaggg ctgcctgggt 60
 gcagttcttg taaccacagga ggaagccac ggctcctctgc accggcgccg gcgcgcaac 120
 gcgttctctg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc 180
 tccttcgagg aggcccgga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240
 tottacagtg atgggggacca gtgtgctctca agtccatgcc agaattgggg ctctctgcaag 300
 gaccagctcc agtctctatat ctgcttctgc ctccctgcct tcgagggcgc gaactgtgag 360
 acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcgctgtgta gcagtactgc 420
 agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgtgtgca 480
 gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa 540
 aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg 600
 gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg 660

```

atcaacacca tctgggtggt ctccggcgcc cactgtttcg acaaaatcaa gaactggagg 720
aacctgatcg cgggtgctggg cgagcacgac ctacgcgagc acgacgggga tgagcagagc 780
cggcggtggt cgcagggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac 840
atcgcgctgc tccgcctgca ccagcccgtg gtectcactg accatgtggt gccctctgctc 900
ctgcccgaac ggaagttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc 960
ggctggggcc agctgctgga cctggcgcc accggccttg agctcatggt gctcaacgtg 1020
ccccgctga tgaccaggga ctgctcgagc cagtcacgga aggtgggaga ctcccacaaat 1080
atcacggagt acatgttctg tgcgggtac tcggatggca gcaaggactc ctgcaagggg 1140
gacagtggag gccacatgc caccactac cggggcagct ggtacctgac gggcatcgctc 1200
agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctccag 1260
tacatcgagt ggctgcaaaa gctcatgctc tcagagccac gccaggaggt cctcctgaga 1320
gccccatttc cc 1332

```

```

<210> 8
<211> 444
<212> PRT
<213> Homo sapiens

```

```

<400> 8
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
1 5 10 15
Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20 25 30
Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45
Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60
Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80
Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95
Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125
Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140
Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160
Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

```

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
 180 185 190
 Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
 195 200 205
 Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
 210 215 220
 Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
 225 230 235 240
 Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
 245 250 255
 Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
 260 265 270
 Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 275 280 285
 Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300
 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415
 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
 420 425 430
 Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
 435 440

<210> 9

<211> 1437

<212> DNA

<213> Homo sapiens

<400> 9

atgcagcgcg tgaacatgat catggcagaa tcaccaagcc tcatcaccat ctgcctttta 60

ggatatctac tcaagtctga atgtacagtt ttctctgata atgaaaacgc caacaaaatt 120

ctgaatcggc caaagaggtta taattcaggt aaattggaag agtttgttca agggaaacctt 180
 gagagagaat gtatggaaga aaagtgtagt ttggaagaac caagagaagt ttttgaaaac 240
 actgaaaaga caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat 300
 ccatgtttaa atggcgccag ttgcaaggat gacattaatt cctatgaatg ttggtgtccc 360
 ttgtgatttg aaggaaagaa ctgtgaatta gatgtaacat gtaacattaa gaatggcaga 420
 tgogagcagt tttgtaaaaa tagtgctgat aacaaggtgg ttgtctctg tactgagggg 480
 tatogacttg cagaaaacca gaagtctgt gaaccagcag tgccatttcc atgtggaaga 540
 gtttctgttt cacaaccttc taagctcacc cgtgctgagg ctgtttttcc tgatgtggac 600
 tatgtaaatc ctaactgaagc tgaaaaccatt ttggataaca tcactcaagg cacccaatca 660
 tttaatgact tcactcgggt tgttgggtgga gaagatgcca aaccaggcca attcctttgg 720
 caggttgttt tgaattgtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa 780
 tggattgtaa ctgctgccca ctgtgttgaa actggtgtta aaattacagt tgcgcagggt 840
 gaacataata ttgaggagac agaacataca gagcaaaagc gaaatgtgat tcgagcaatt 900
 attcctcacc acaactacaa tgcagctatt aataagtaca accatgacat tgcccctctg 960
 gaactggagc aaoccttagt gctaaacagc tacgttacac ctatttgcatt tgctgacaag 1020
 gaatacacga acatcttctt caaatttgga tctggctatg taagtggctg ggcaagagtc 1080
 ttccacaaag ggagatcagc tttagttctt cagtacctta gagttccact tgttgaccga 1140
 gccacatgtc ttgatctac aaagtccacc atctataaca acatgttctg tgctggcttc 1200
 catgaaggag gtgagagatc atgtcaagga gatagtggg gaccocatgt tactgaagtg 1260
 gaagggacca gtttcttaac tggaattatt agctggggtg aagagtgtgc aatgaaaggc 1320
 aaatattgaa tatataccaa ggtatccogg tatgtcaact ggattaagga aaaaaccaag 1380
 ctacctaatt gaaagatgga ttccaaggt taattcattg gaattgaaaa ttaacag 1437

<210> 10
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr
 1 5 10 15
 Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
 20 25 30
 Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
 35 40 45
 Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys

50	55	60
Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn 65 70 75 80		
Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln 85 90 95		
Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile 100 105 110		
Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys 115 120 125		
Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe 130 135 140		
Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly 145 150 155 160		
Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe 165 170 175		
Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala 180 185 190		
Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu 195 200 205		
Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe 210 215 220		
Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp 225 230 235 240		
Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile 245 250 255		
Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly 260 265 270		
Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu 275 280 285		
His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His 290 295 300		
Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu 305 310 315 320		
Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys 325 330 335		
Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly 340 345 350		
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu 355 360 365		
Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu 370 375 380		

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
450 455 460

<210> 11
<211> 603
<212> DNA
<213> Homo sapiens

<400> 11
atggattact acagaaaata tgcagctatc ttcttggtca cattgtcgtt gttcttgcac 60
gtttccatt ccgtctctga tgtgcaggat tgcccagaat gcacgtcaca ggaaaaccca 120
ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca 180
tatccactc cactaagtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240
tcacattgct gtgtagctaa atcatataac agggtcacag taatgggggg tttaaagtgt 300
gagaaccaca cggcgtgcc ctgcagtact tgttattatc acaaatotta aatgttttac 360
caagtgcgtt ctgtgatgact gctgattttc tggaatggaa aattaagttg ttagtggtt 420
atggccttgt gagataaac tctctcttct cttaccatac cactttgaca cgcttcaagg 480
atatactgca gcttactgc cttctcctt atctacagc acaatcagca gctagttct 540
tttcatttgg aatgaataca gcattaagct tgttccactg caaataaagc cttttaaatc 600
atc 603

<210> 12
<211> 116
<212> PRT
<213> Homo sapiens

<400> 12
Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1 5 10
Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
20 25 30
Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
35 40 45
Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
100 105 110

Tyr His Lys Ser
115

<210> 13
<211> 390
<212> DNA
<213> Homo sapiens

<400> 13
atgaagacac tccagttttt ctctcttttc tgtgctgga aagcaatctg ctgcaatagc 60
tgtgagctga ccaacatcac cattgcaata gagaagaag aatgtcggtt ctgcataagc 120
atcaacacca ctgtggtgtgc tggctactgc tacaccaggg atctggtgta taaggaccca 180
gccaggccca aaatccagaa aacatgtacc ttcaaggaa tggtatatga aacagtgaga 240
gtgcccggt gtgctcacca tgcagattcc ttgtatacat acccagtggc caccagtggt 300
cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggccacgc 360
tactgtctct ttggtgaat gaaagaataa 390

<210> 14
<211> 129
<212> PRT
<213> Homo sapiens

<400> 14
Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys

115

120

125

Glu

```

<210> 15
<211> 1342
<212> DNA
<213> Homo sapiens

<400> 15
cccgagccg gaccggggcc accgcgccg ctctgctccg acaccgcc ccctggacag 60
ccgccctctc ctccaggccc gtggggctgg cctgcacccg ccgagcttcc cgggatgagg 120
gcccccggtg tggtcacccg gcgcgcacca ggtcgctgag ggaccccggc caggcgcgga 180
gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgctccc 240
tctgggcctc ccagtctcgg gcgccccacc acgcctcacc tgtgacagcc gagtccctgga 300
gaggtagctc ttggaggcca aggaggccga gaatatcacg acgggctgtg ctgaacactg 360
cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag 420
gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc 480
tgtcctgcgg ggcacaggccc tgttggtcaa ctcttcccag ccgtgggagc cctgcagct 540
gcatgtggat aaagccgtca gtggccttcg cagcctcacc actctgcttc gggctctgcg 600
agcccagaag gaagccatct cccctccaga tgcggcctca gctgctccac tcggaacaat 660
cactgctgac actttccgca aactcttccg agtctaactc aatttctcc ggggaaagct 720
gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccaggtg tgtccacctg 780
ggcatatcca ccacctccct caccaacatt gcttgtgcca caccctcccc gcgcactcct 840
gaaccccgtc gaggggctct cagctcagcg ccagcctgtc ccattggacac tccagtgtcca 900
gcaatgacat ctacggggcc agagggaactg tccagagagc aactctgaga tctaaggatg 960
tcacagggcc aacttgaggg ccagagcagc gaagcattca gagagcagct ttaactcag 1020
ggacagagcc atgctgggaa gacgcctgag ctcaactcggc accctgcaaa atttgatgcc 1080
aggacacgct ttggaggcga tttaactgtt ttgcaccta ccatcaggga caggatgacc 1140
tggagaactt agtgggcaag ctgtgacttc tccaggctc acgggcattg gcaactccctt 1200
ggtggcaaga gcccccctga cacgggggtg gtgggaacca tgaagacagg atgggggctg 1260
gcctctggct ctcatggggt ccaagttttg tgtattcttc aaactcattg acaagaactg 1320
aaaccaccaa aaaaaaaaaa aa 1342

<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

```

<400> 16

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Arg

<210> 17

<211> 435

<212> DNA

<213> Homo sapiens

<400> 17

atgtggtgc agagcctgct gctcttgggc actgtggcct gcagcatctc tgcacccgcc 60
 cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggagggccgg 120
 cgtctctga acctgagtag agacactgct gctgagatga atgaacacagt agaagtcac 180
 tcagaaatgt ttgacctoca ggagccgacc tgcctacaga cccgctcgga gctgtacaag 240
 cagggcctgc ggggcagcct caccaagctc aagggcccct tgaccatgat ggccagccac 300
 tacaagcagc actgccctcc aaccccggaa acttctctgt caaccacagat tatcaccttt 360
 gaaagtttca aagagaacct gaaggacttt ctgcttgtca tcccctttga ctgctgggag 420

ccagtcacgg agtga

435

<210> 18
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
 1 5 10 15
 Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
 20 25 30
 Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
 35 40 45
 Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
 50 55 60
 Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
 65 70 75 80
 Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
 85 90 95
 Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
 100 105 110
 Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
 115 120 125
 Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 130 135 140

<210> 19
 <211> 501
 <212> DNA
 <213> Homo sapiens

<400> 19
 atgaaatata caagttatat cttggctttt cagctctgca tcgttttggg ttctcttggc 60
 tgttactgcc aggaccata tgtaaaagaa gcagaaaacc ttaagaaata ttttaatgca 120
 ggctattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180
 gaggagagtg acagaaaaat aatgcagagc caaattgtct ccttttactt caaacttttt 240
 aaaaacttta aagatgacca gagcatocaa aagagtgtgg agaccatcaa ggaagacatg 300
 aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360
 tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg 420
 gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480
 ggctgaagag catcccagta a 501
 <210> 20
 <211> 166

<212> PRT

<213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
20 25 30Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
35 40 45Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
50 55 60Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65 70 75 80Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
85 90 95Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
100 105 110Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
115 120 125Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
130 135 140Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145 150 155 160Gly Arg Arg Ala Ser Gln
165

<210> 21

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 21

ctgggacagt gaatcgacaa tgcgctcttc tgtctcgtgg ggcacccctc tgctggcagc 60

cctgtgtctgc ctggtccctg tctccctggc tgaggatccc caggagatg ctgccacaga 120

gacagatata tcccaccatg atcaggatca cccaaccttc aacaagatca cccccaacct 180

ggctgagttc gccttcagcc tataccgaca gctggcacac cagtccaaca gcaccaatat 240

cttctctctc ccagtgagca togctacagc ctttgcaatg ctctccctgg ggaccaaggc 300

tgacaactca gatgaaatcc tggaggggcct gaatttcaac ctacaggaga ttccggaggc 360

tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct 420

ccagctgacc acocggcaatg gcctgttccct cagcgagggc ctgaagctag tggataagtt 480

tttgagggat gttaaaaagt tgtaccacto agaagccttc actgtcaact tcggggacac 540

cgaagaggcc aagaacacaga tcaacgatta cgtggagaag ggtactcaag ggaaatgtgt 600
 ggatttggtc aaggagcttg acagagacac agtttttctg ctggtgaatt acatcttctt 660
 taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt 720
 ggaccagggtg accaccgtga aggtgcctat gatgaagcgt ttaggcatgt ttaacatcca 780
 gcactgtaag aagctgtcca gctgggtgct gctgatgaaa tacctgggca atgccaccgc 840
 catcttcttc ctgcctgatg aggggaaact acagcacctg gaaaatgaac tcaccacga 900
 tatcatcacc aagtctctgg aaaatgaaga cagaaggtct gccagcttac atttaccxaa 960
 actgtocatt actggaacct atgatctgaa gagcgtcctg ggccaactgg gcatactaa 1020
 ggtcttcagc aatggggctg acctctccgg ggtcacagag gaggcacccc tgaagctctc 1080
 caaggccgtg cataaggctg tgctgacctat cgacgagaaa gggactgaag ctgctggggc 1140
 catgttttta gagggcctac ccattgtctat ccccccgag gtcaagtcca acaaacctt 1200
 tgtctcttta atgattgaac aaaataccaa gtctccctc ttcatgggaa aagtgggtgaa 1260
 tocccaccaa aaataactgc ctctcgctcc tcaacccctc ccctccatcc ctggccccct 1320
 cctggatga cattaagaa gggttgagct gg 1352

<210> 22
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Ala Gly Leu Cys
 1 5 10 15
 Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
 20 25 30
 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 35 40 45
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 50 55 60
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 65 70 75 80
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 85 90 95
 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
 100 105 110
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 115 120 125
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 145 150 155 160
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 165 170 175
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 180 185 190
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 195 200 205
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 210 215 220
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
 225 230 235 240
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 245 250 255
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 260 265 270
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 275 280 285
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 290 295 300
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 305 310 315 320
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 325 330 335
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 340 345 350
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 355 360 365
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 370 375 380
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 385 390 395 400
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 405 410 415
 Gln Lys
 <210> 23
 <211> 2004
 <212> DNA
 <213> Homo sapiens
 <400> 23
 gctaacctag tgcctatagc taaggcaggt acctgcatcc ttgtttttgt ttatgggatc 60

ctctatcctt cagagactct ggaacccttg tggctctctc ttcattataat gaccttgagg 120
 ggatggagtt ttcaagtctt tcacagagagg aatgtcccaa gcctttgagt agggtaagca 180
 tcatggcttg cagcctcaca ggtttgcttc tacttcaggc agtgctctgg gcatcaggtg 240
 cccgcccttg catccctaaa agcttcggct acagctcggg ggtgtgtgtc tgcattgcca 300
 catactgtga ctcccttgac ccccgacct ttcttgccct tggtaacctc agccgctatg 360
 agagtacacg cagtgggcga cggatggagc tgagtatggg gcccatccag gctaatacaca 420
 cgggcacagg cctgctactg aacctgcagc cagaacagaa gttccagaaa gtgaagggat 480
 ttggaggggc catgacagat gctgctgtct tcaacatcct tgccctgtca cccctgtccc 540
 aaaatttgct acttaaatcg tacttctctg aagaaggaat cggatataac atcatccggg 600
 taoccatggc cagctgtgac ttctccatcc gcacctacac ctatgcagac acccctgatg 660
 atttccagtt gcacaacttc agcctcccag aggaagatag caagctcaag atacctctga 720
 ttacccgagc cctgcagttg gccagcgtc ccgtttcact ccttgccagc ccctggacat 780
 caoccatctg gctcaagacc aatggagcgg tgaatgggaa ggggtcactc aaggacagc 840
 ccggagacat ctaccaccag aacctgggca gatactttgt gaagtctctg gatgcctatg 900
 ctgagcaciaa gttacagttc tgggcagtg cagctgaaaa tgagccttct gctgggctgt 960
 tgagtggata ccccttccag tgccctggct tcacctctga acatcagcga gacttcattg 1020
 ccgtgacct aggtcctacc ctogccaaca gtactcaaca caatgtccgc ctactcatgc 1080
 tggatgacca acgcttgctg ctgcccact gggcaaaagt ggtactgaca gaccagaag 1140
 cagctaaata tgttcatggc attgctgtac attggtacct ggaatttctg gctccagcca 1200
 aagccacct aggggagaca caccgctgt tcccaaacac catgctcttt gctcagagg 1260
 cctgtgtggg ctccaagttc tgggagcaga gtgtgcggct aggetcctgg gatcagagg 1320
 tgcagtacag ccacagcacc atccgaacc tctgtacca tgtgttcggc tggacagact 1380
 ggaaccttgc cctgaacccc gaaggaggac ccaattgggt gcgtaaactt gtcgacagtc 1440
 ccactattgt agacatcacc aaggacacgt ttacaaaaca gccatgttc taaccacttg 1500
 gccacttcag caagttcatt cctgagggtc ccagagagt ggggctgggt gccagtcaga 1560
 agaacgacct ggacgcagtg gactgatgc atccgatgg ctctgtgttt gtggtcgtgc 1620
 taaaccgtct ctctaaggat gtgcctctta ccataaggga tctgtgtgtg ggcttcttg 1680
 agacaatctc acctggctac tccattcaca cctacctgtg gcatcgccag tgatggagca 1740
 gatactcaag gaggcacttg gctcagcctg ggcattaaag ggacagagtc agctcacacg 1800
 ctgtctgtga ctaaaagggg cacagcaggg ccagtgtgag cttacagcga cgtaaagcca 1860
 ggggcaatgg tttgggtgac tcaatttccc ctctaggtgg tgccaggggc tggaggcccc 1920

tagaaaaaga tcagtaagcc ccagtgcccc ccagccccc atgettattgt gaacatgcgc 1980
 tgtgtgctgc ttgctttgga aact 2004

<210> 24
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
 1 5 10 15
 Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
 20 25 30
 Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45
 Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60
 Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
 65 70 75 80
 Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
 85 90 95
 Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110
 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125
 Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140
 Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160
 Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175
 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190
 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205
 Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
 210 215 220
 Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
 225 230 235 240
 Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
 245 250 255
 Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
 260 265 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
275 280 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
290 295 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
305 310 315 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
325 330 335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
340 345 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
355 360 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
370 375 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
385 390 395 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
405 410 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
420 425 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
435 440 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
450 455 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
465 470 475 480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
485 490 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
500 505 510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
515 520 525

His Thr Tyr Leu Trp His Arg Gln
530 535

<210> 25

<211> 1726

<212> DNA

<213> Homo sapiens

<400> 25

atggatgcaa tgaagagag gctctgctgt gtgctgctgc tgtgtggagc agtcttcggt 60

tgcgccagcc aggaatcca tgcccgattc agaagaggag ccagatetta ccaagtgatc 120

tgacagatg	aaaaaacgca	gatgatatac	cagcaacatc	agtcattggt	gcgcctctgt	180
ctcagaagca	acgggttgga	atattgctg	tgcaacagt	gcagggcaca	gtgccactca	240
gtgcctgtca	aaagttgcag	cgagccaag	tgtttcaacg	ggggcacctg	ccagcaggcc	300
ctgtacttct	cagatttctg	gtgccagtgc	ccgaaggat	ttgctgggaa	gtgctgtgaa	360
atagatacca	gggccacgtg	ctacaggagc	cagggcatca	gctacagggg	cactgtggagc	420
acagcggaga	gtggcgccga	gtgcaccaac	tggaacagca	gcgcgttgcc	ccagaagccc	480
tacagcgggc	ggaggccaga	cgccatcagg	ctgggcctgg	ggaaccacaa	ctactgcaga	540
aaaccagatc	gagactcaaa	gccctgggtg	tacgtcttta	aggcggggaa	gtacagctca	600
gagttctgca	gcacccctgc	ctgctctgag	ggaacagtgc	actgctactt	tggaatggg	660
tcagcctacc	gtggcacgca	cagcctcacc	gagtcgggtg	cctcctgcct	cccggtgaat	720
tcctatgatc	tgataggcaa	ggtttacaca	gcacagaacc	ccagtgccca	ggcactgggc	780
ctgggcaaac	ataattactg	ccggaatcct	gatggggatg	ccaagccctg	gtgccacgtg	840
ctgaagaacc	gcaggctgac	gtgggagtag	tgtgatgtgc	cctcctgctc	cacctgcggc	900
ctgagacagt	acagccagcc	tcagttttcg	atcaaaggag	ggctcttctg	cgacatcgcc	960
tcccacccct	ggcaggctgc	catctttgcc	aagcacagga	ggtcgccggg	agagcgggtc	1020
ctgtgcgggg	gcatactcat	cagctcctgc	tggattctct	ctgcgcacca	ctgcttccag	1080
gagagggttc	cgccccacca	cctgacgggt	atcttgggca	gaacataccg	ggtagtccct	1140
ggcgaggagg	agcagaaatt	tgaagtogaa	aaatacatgt	tcataaagga	attcgatgat	1200
gacacttacg	acaatgacat	tgcgctgctg	cagctgaaat	cggattcgtc	ccgctgtgcc	1260
caggagagca	gcgtgggtcc	cactgtgtgc	cttccccggg	cggacctgca	gctgcgggac	1320
tggacggagt	gtgagctctc	cggctacggc	aagcatgagg	ccttgtctcc	tttctattcg	1380
gagcggctga	aggaggctca	tgctcagact	taccatcca	gcgcgtgcac	atcacacat	1440
ttacttaaca	gaacagtca	cgacaacatg	ctgtgtgctg	gagacactcg	gagcggcggg	1500
ccccaggcaa	acttgacaga	cgccctccag	ggcgattcgg	gaggccccct	ggtgtgtctg	1560
aacgatggcc	gcattgactt	ggtgggcctc	atcagctggg	gcctgggctg	tggacagaag	1620
gatgtcccg	gtgtgtacac	caaggttacc	aactacctag	actggattcg	tgacaacatg	1680
cgacctgac	cagggaacacc	cgactcctca	aaagcaaatg	agatcc		1726

<210> 26
 <211> 562
 <212> PRT
 <213> Homo sapiens
 <400> 26

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
 20 25 30
 Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
 35 40 45
 Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
 50 55 60
 Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
 65 70 75 80
 Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
 85 90 95
 Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
 100 105 110
 Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
 115 120 125
 Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
 130 135 140
 Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
 145 150 155 160
 Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
 165 170 175
 Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
 180 185 190
 Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
 195 200 205
 Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
 210 215 220
 Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
 225 230 235 240
 Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
 245 250 255
 Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
 260 265 270
 Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
 275 280 285
 Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr
 290 295 300
 Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala
 305 310 315 320
 Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro

400> 27	atcactctct ttaatacacta ctcacattaa cctcaactcc tgcacacagt tacaggatgc	60
	aactcctctgc ttgcattgca ctaattcttg cacttgtcac aaacagtgca cctacttcaa	120
	gttcgcacaa gaaaacaacag aaaacacagc tacaactgga gcatttaagt ctggatttac	180
	agatgatgtt gaatggaatt aataattaca agaatcccaa actcaccagg atgtccacat	240
	ttaagtttta catgcccaag aaggccacag aactgaacaa ctttcagtgt ctagaagaag	300

```

aactcaaacc tctggaggaa gtgctgaatt tagctcaaag caaaaacttt cacttaagac 360
ccagggaatt aatcagcaat atcaacgtaa tagttctgga actaaaggga tctgaacaa 420
cattcatgtg tgaatatgca gatgagacag caaccattgt agaatttctg aacagatgga 480
ttaccttttg tcaaagcatc atctcaacac taacttgata attaatgtct tcccaactaa 540
aacatatcag gcctcttatt tattttatta aatattttaa ttttatattt attgttgaat 600
gtatgggtgc tacctattgt aactattatt cttaacttta aaactataaa tatggatctt 660
ttatgattct ttttgtaagc cctaggggct ctaaaatggt ttaccttatt tatccaaaa 720
atatttatta ttatgttgaa tgttaaatat agtatctatg tagattgggt agtaaaacta 780
tttaataaat ttgataaata taataaaaaa aaacaaaaaa aaaaa 825

```

```

<210> 28
<211> 156
<212> PRT
<213> Homo sapiens

```

```

<400> 28
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu
1 5 10 15
Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys
20 25 30
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
35 40 45
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
50 55 60
Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln
65 70 75 80
Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
85 90 95
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
100 105 110
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
115 120 125
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
130 135 140
Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
145 150 155

```

```

<210> 29
<211> 7931
<212> DNA
<213> Homo sapiens

```

```

<400> 29

```

atgcaaatag agctctccac ctgcttcttt ctgtgccttt tgcgattctg ctttagtgcc	60
accagaagat actacctggg tgcagtgga ctgtcatggg actatatgca aagtgatctc	120
ggtgagctgc ctgtggacgc aagatttctt cctagagtgc caaaatcttt tccattcaac	180
acctcagtcg tgtacaaaa gactctgttt gtagaattca cggatcacct tttaacatc	240
gctaagccaa ggccaccctg gatgggtctg ctaggtccta ccatccaggc tgaggtttat	300
gatacagtgg tcaattacact taagaacatg gcttcccatc ctgtcagtct tcatgctgtt	360
ggtgtatcct actggaaagc ttctgagggg gctgaatatg atgatcagac cagtc aaagg	420
gagaaagaag atgataaagt ctccctgggt ggaagccata catatgtctg gcaggctctg	480
aaagagaatg gtccaatggc ctctgaccca ctgtgcctta cctactcata tctttctcat	540
gtggacctg taaaagactt gaattcaggc ctcatggag ccctactagt atgtagagaa	600
gggagtctgg ccaaggaaaa gacacagacc ttgcacaaat ttatactact ttttctgtta	660
tttgatgaag ggaaaagtgt gcaactcagaa acaagaact ccttgatgca ggatagggat	720
gtgtcatctg ctctgggctg gccaaaaatg cacacagtca atggttatgt aaacaggtct	780
ctgccaggtc tgattggatg ccacaggaaa tcagttctatt ggcatgtgat tggaatgggc	840
accactctg aagtgcactc aatattcttc gaaggtcaca cattttctgt gaggaacct	900
ogccaggcgt ccttggaat ctgcgaata actttcctta ctgctcaaac actcttgatg	960
gaccttgac agtttctact gttttgtcat atctcttccc accaacaatga tggcatggaa	1020
gcttatgtca aagtagacag ctgtccagag gaaccccaac tacgaatgaa aataatgaa	1080
gaagcggaag actatgatga tgatcttact gattctgaaa tggatgtggt caggtttgat	1140
gatgacaact ctcttctctt tatccaatt cgctcagttg ccaagaagca tcttaaaact	1200
tgggtacatt acattgtctc tgaagaggag gactgggact atgtctcctt agtcctcgcc	1260
cccgatgaca gaagtataa aagtcaatat ttgaacaatg gccctcagcg gattggtagg	1320
aagtacaaaa aagtcagatt tatggcatac acagatgaaa cctttaagac togtgaagct	1380
attcagcatg aatcaggaat cttgggacct ttactttatg gggaagtgg agacacactg	1440
ttgattatat ttaagaatca agcaagcaga ccatataaca tctacctca cggaaact	1500
gatgtccgtc ctttgtattc aaggagatta ccaaaagggtg taaaacattt gaaggatttt	1560
ccaattctgc caggagaaat attcaaatat aaatggacag tgactgtaga agatggccca	1620
actaaatcag atctcgggtg cctgaccgcg tattactcta gtttcgttaa tatggagaga	1680
gactatagct caggactcat tggccctctc ctcatctgct acaagaatc tgtagatcaa	1740
agaggaaacc agataatgtc agacaagggt aatgtcatcc tgttttctgt atttgatgag	1800
aaccgaagct ggtacctcac agagaatata caacgcttct tccccatcc agctggagtg	1860

cagccttgagg atccagaggtt ccaagcctcc aacatcatgc acagcatcaa tggctatggt 1920
 tttagatggt tgcagttgtc agtttgtttg catgaggttg catactggta cattotaaagc 1980
 attggagcac agactgaact cctttctgtc ttcttctctg gatatacctt caaacacaaa 2040
 atggtctatg aagacacact caccctattc coattctcag gagaactgt cttcatgtcg 2100
 atgaaaaacc caggctctatg gattctgggg tgcacaact cagactttcg gaacagaggc 2160
 atgaccgcct tactgaagggt ttctagtgtg gacaagaaca ctggtgatta ttaacaggagc 2220
 agttatgaag atatttcagc ataactgtcg agtaaaaaa atgccattga accaagaagc 2280
 ttctcccaga attcaagaca ccgtagcact aggcacaaa aatttaatgc caccacaatt 2340
 ccagaaaatg acatagagaa gactgacctt tggtttgac acagaacacc tatgcctaaa 2400
 atacaaaatg tctctctag tgatttgttg atgctcttg gacagagtc tactccacat 2460
 gggtatcct tatctgatct ccaagaagcc aaatatgaga ctttttctga tgatcatca 2520
 cctggagcaa tagacagtaa taacagcctg tctgaaatga cacacttcag gccacagctc 2580
 catcacagtg gggacatggt atttaccctt gagtcaggcc tccaattaa attaaatgag 2640
 aaactgggga caactgcagc aacagagttg aagaaacttg atttcaaagt ttctagtaca 2700
 tcaataatc tgatttcaac aattccatca gacaatttgg cagcaggtag tgataatata 2760
 agttccttag gacccccag tatgccagtt cattatgata gtcaattaga taccactcta 2820
 ttgggcaaaa agtcatctcc ccttactgag tctgggtggac ctctgagctt gagtgaagaa 2880
 aataatgatt caaagttggt agaatcaggt ttaatgaata gccaaagaa ttcatgggga 2940
 aaaaatgtat cgtcaacaga gagtggtagg ttattttaa ggaaaagagc tcatggacct 3000
 gctttgttga ctaaagataa tgccttattc aaagttagca tctctttgtt aaagacaaac 3060
 aaaacttcca ataattcagc aactaataga aagactcaca ttgatggccc atcattatta 3120
 attgagaata gtccatcagt ctggcaaaat atattagaaa gtgacctga gtttaaaaaa 3180
 gtgacacctt tgattcatga cagaatgctt atggacaaaa atgctacagc tttagggcta 3240
 aatcatatgt caataaaaa tacttcatca aaaaacatgg aaatggtcca acagaaaaaa 3300
 gagggcccca ttccaccaga tgcacaaaat ccagatatgt cgttctttaa gatgctattc 3360
 ttgcagaat cagcaagggt gatcaaaag actcatggaa agaactctct gaactctggg 3420
 caaggcccca gtccaaagca attagtatcc ttaggaccag aaaaatctgt ggaaggtcag 3480
 aatttcttgt ctgagaaaaa caaagtggtg taggaaagg gtgaatttac aaaggacgta 3540
 ggactcaaag agatgggttt tocaagcagc agaaacctat ttcttactaa cttggataat 3600
 ttacatgaaa ataatacaca caatcaagaa aaaaaaattc aggaagaaat agaaaagaag 3660

gaacatttaa tccaagagaa ttagttagttt cctcagatag atcagtgac tggcactaag 3720
 aatttcatga agaaaccttt cttactgagc actaggcaaa atgtagaagg ttcattatgac 3780
 ggggcatatg ctccagtact tcaagatttt aggtcattaa atgattcaac aaatagaaca 3840
 aagaaacaca cagctcattt ctcaaaaaaa ggggaggaag aaaacttgga aggtctggga 3900
 aatcaaacca agcaaatgtg agagaaatat gcatgcacca caaggatata tctaatata 3960
 agccagcaga attttgcac gcaacgtagt aagagagctt tgaacaatt cagactccca 4020
 ctagaagaaa cagaacttga aaaaagata attgtggatg acacctcaac ccagtgtcc 4080
 aaaaacatga aacatttgac ccgagcacc ctccacaga tagactacaa tgagaaggag 4140
 aaagggcca tttactcagc tccctatca gattgcctta cgaggagtca tagcatccct 4200
 caagcaaatg gatctccatt acccattgca aaggtatcat catttccatc tattagacct 4260
 atatatctga ccagggtcct attccaagac aactctctc atcttccagc agcatcttat 4320
 agaaagaaag attctgggtt ccaagaagac agtcatttct tacaaggagc caaaaaaat 4380
 aacctttctt tagcattctt aaccttgag atgactggtg atcaagaga ggttggtccc 4440
 ctggggcaaa gtgccacaaa ttcagtcaca tacaagaaag ttgagaacac tgttctccc 4500
 aaaccagact tgcccaaaa atctggcaaa gttgaattgc tccaaaagt tcacatttat 4560
 cagaaggacc tttccctac ggaaactagc aatgggtctc ctggccatct ggtctctgtg 4620
 gaagggagcc tcttcaggg aacagaggga gcgattaagt ggaatgaagc aaacagacct 4680
 ggaaaagttc ctttctgag agtagcaaca gaaagctctg caaagactcc ctccaagcta 4740
 ttgtagcttc ttgcttgga taacctatg ggtactcaga taccaaaaga agagtggaaa 4800
 tccaagaga agtcaccaga aaaaacagct ttaagaaaa aggataccat tttgacctg 4860
 aacgttctgt aaagcaatca tgcaatagca gcaataatg agggacaaaa taagcccgaa 4920
 atagaagtca ctggggcaaa gcaagtagg actgaaaggc tgtgctctca aaaccacca 4980
 gtcttgaac gccatcaacg ggaataact cgtactactc ttcagtcaga tcaagaggaa 5040
 attgactatg atgataccat atcagttgaa atgaagaag aagatttga catttatgat 5100
 gaggatgaaa atcagagccc ccgagcttt caaaagaaaa cagacacta ttttattgct 5160
 gcagtggaga ggctctggga ttatgggatg agtagctccc cacatgttct aagaacacag 5220
 gtcagagtg gcaggtccc tcagttcaag aaagttgtt tccaggaatt tactgatggc 5280
 tctttactc agcccttata ccgtggagaa ctaaatgaac atttgggact cctggggcca 5340
 tatataagag cagaagtga agataatac atggtaactt tcagaaatca ggctctctgt 5400
 cctatttct tctattctag cttatttct tatgaggaag atcagaggca aggagcagaa 5460
 cctagaaaaa actttgtcaa gctaatgaa accaaaactt acttttgaa agtgcaacat 5520

catatggcac ccactaaaga tgagtttgac tgcaaacctt gggcttattt ctctgatgtt 5580
 gacctgaaaa aagatgtgca ctcaggcctg attggacccc ttctggctctg ccactactaa 5640
 aactgaacc ctgctcatgg gagacaagtg acagtacagg aatttgctct gtttttcacc 5700
 atctttgatg agacaaaag ctggtacttc actgaaaaa tgaaagaaa ctgcagggct 5760
 cctgcgaata tccagatgga agatccact tttaaagaga attatcgctt ccatgcaato 5820
 aatggctaca taetggatc actacctggc ttagtaatgg ctcaggatca aaggattcga 5880
 tggatatctg tcagcatggg cagcaatgaa aacatccatt ctattcattt cagtggacat 5940
 gtgttcactg tacgaaaaa agaggagtat aaaatggcac tgtacaatct ctatccaggt 6000
 gtttttgaga cagtggaaat gttaccatcc aaagctggaa tttggcgggt ggaatgcctt 6060
 attggcgagc atctacatgc tgggatgagc acacttttct tgggtgacag caataagtg 6120
 cagaactccc tgggaatggc ttctggacac attagagatt ttcagattac agcttcagga 6180
 caatatggac agtgggcccc aaagctggcc agacttcatt attccggatc aatcaatgcc 6240
 tggagacca aggagccctt ttcttggatc aaggtggatg tgttggcacc aatgattatt 6300
 caggcatca agacccaggg tgcccgctag aagtctcca gcctctacat ctctcagttt 6360
 atcatcatgt atagtcttga tgggaagaag tggcagactt atcagaggaa ttcaactgga 6420
 accttaatgg tcttctttgg caatgtggat tcatotggga taaaacacaa tatttttaac 6480
 cctccaatta ttgctcgata catccgtttg caccacaact attatagcat tcgcagcaat 6540
 ctctcgatgg agttgatggg ctgtgattta aatagttgca gcatgccatt ggggaatggag 6600
 agtaaagcaa tatcagatgc acagattact gcttcactct actttaccaa tatgtttgcc 6660
 acctggtctc cttcaaaagc tcgaactcac ctccaaggga ggagtaatgc ctggagacct 6720
 caggtgaata atccaaaaga gtgggtgcaa gtggacttcc agaagacaat gaaagtcaca 6780
 ggagtaacta ctcaggaggat aaaatctctg cttaccagca tgtatgtgaa ggagttcttc 6840
 atctccagca gtcaagatgg ccatcagttg actctctttt ttcagaatgg caaagtaaa 6900
 gtttttcagg gaaatcaaga ctcttccaa cctgtgttga actctctaga cccaccgtta 6960
 ctgaotcgct accttcgaat tcaccccccag agttgggtgc accagattgc cctgaggatg 7020
 gaggttctgg gctgcgaggg acaggacctc tactgagggg ggccactgca gcacctgca 7080
 ctgccgtcac ctctccctcc tcagctccag ggcagtgctc ctccctggct tgccctctac 7140
 ctttgtgcta aatcctagca gacactgcct tgaagcctcc tgaattaact atcatcagtc 7200
 ctgcatttct ttggtggggg gccaggaggg tgcacccaat ttaacttaac tcttacctat 7260
 tttctgcagc tgcctccaga ttactccttc ctccaatat aactaggcaa aaagaagtga 7320

ggagaaacct gcatgaaagc attcttcctt gaaaagttag gcctctcaga gtcaccactt 7380
 cctctgttgt agaaaaacta tgtgatgaaa ctttgaaaaa gatatttatg atgttaacat 7440
 ttcagggttaa gcctcatacg tttaaaataa aactctcagt tgtttattat cctgatcaag 7500
 catggaacaa agcatgttct aggatcagat caatacaatc ttggagtc aaaggcaaatc 7560
 atttgacaaa tctgcaaaaat ggagagaata caataactac tacagtaaag tctgtttctg 7620
 ctcccttaca catagatata attatgttat ttatgcatta tgagggggcac attcttatct 7680
 ccaaaactag cattottaaa ctgagaatta tagatggggg tcaagaatcc ctaagtcccc 7740
 tgaattata taaggcattc tgtataaatg caaatgtgca tttttctgac gagtgtccat 7800
 agatataaag ccatttggct ttaattctga ccaataaaaa aataagtcag gaggatgcaa 7860
 ttgttgaaag ctttgaaata aaataacaat gtcttcttga aatttgtgat ggccaagaaa 7920
 gaaatgatg a 7931

<210> 30
 <211> 2351
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
 1 5 10 15
 Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
 20 25 30
 Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
 35 40 45
 Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
 50 55 60
 Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
 65 70 75 80
 Ala Lys Pro Arg Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
 85 90 95
 Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
 100 105 110
 His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
 115 120 125
 Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
 130 135 140
 Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
 145 150 155 160
 Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
 165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
 180 185 190
 Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
 195 200 205
 Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
 210 215 220
 Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
 225 230 235 240
 Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
 245 250 255
 Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
 260 265 270
 Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
 275 280 285
 Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
 290 295 300
 Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
 305 310 315 320
 Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
 325 330 335
 Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
 340 345 350
 Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
 355 360 365
 Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
 370 375 380
 Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
 385 390 395 400
 Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
 405 410 415
 Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
 420 425 430
 Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
 435 440 445
 Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
 450 455 460
 Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
 465 470 475 480
 Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
 485 490 495
 His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys

500										505										510									
Gly Val Lys His Leu Lys Asp Phe	Pro Ile Leu Pro Gly Glu Ile Phe																												
515	520																												
Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly	Pro Thr Lys Ser Asp																												
530	535																												
Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg																													
545	550																												
Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu																													
565	570																												
Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val																													
580	585																												
Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu																													
595	600																												
Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp																													
610	615																												
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val																													
625	630																												
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp																													
645	650																												
Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe																													
660	665																												
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr																													
675	680																												
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro																													
690	695																												
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly																													
705	710																												
Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp																													
725	730																												
Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys																													
740	745																												
Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg																													
755	760																												
Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp																													
770	775																												
Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys																													
785	790																												
Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser																													
805	810																												
Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr																													
820	825																												

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
 835 840 845
 Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
 850 855 860
 Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
 865 870 875 880
 Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
 885 890 895
 Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
 900 905 910
 Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Ser Ser Met
 915 920 925
 Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
 930 935 940
 Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
 945 950 955 960
 Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
 965 970 975
 Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
 980 985 990
 Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
 995 1000 1005
 Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser
 1010 1015 1020
 Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser
 1025 1030 1035
 Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu
 1040 1045 1050
 Ser Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg
 1055 1060 1065
 Met Leu Met Asp Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met
 1070 1075 1080
 Ser Asn Lys Thr Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln
 1085 1090 1095
 Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met
 1100 1105 1110
 Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile
 1115 1120 1125
 Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro
 1130 1135 1140

Ser Pro	Lys Gln	Leu Val	Ser	Leu Gly	Pro Glu	Lys	Ser Val	Glu
1145			1150			1155		
Gly Gln	Asn Phe	Leu Ser	Glu	Lys Asn	Lys Val	Val	Val Gly	Lys
1160			1165			1170		
Gly Glu	Phe Thr	Lys Asp	Val	Gly Leu	Lys Glu	Met	Val Phe	Pro
1175			1180			1185		
Ser Ser	Arg Asn	Leu Phe	Leu	Thr Asn	Leu Asp	Asn	Leu His	Glu
1190			1195			1200		
Asn Asn	Thr His	Asn Gln	Glu	Lys Lys	Ile Gln	Glu	Glu Ile	Glu
1205			1210			1215		
Lys Lys	Glu Thr	Leu Ile	Gln	Glu Asn	Val Val	Leu	Pro Gln	Ile
1220			1225			1230		
His Thr	Val Thr	Gly Thr	Lys	Asn Phe	Met Lys	Asn	Leu Phe	Leu
1235			1240			1245		
Leu Ser	Thr Arg	Gln Asn	Val	Glu Gly	Ser Tyr	Asp	Gly Ala	Tyr
1250			1255			1260		
Ala Pro	Val Leu	Gln Asp	Phe	Arg Ser	Leu Asn	Asp	Ser Thr	Asn
1265			1270			1275		
Arg Thr	Lys Lys	His Thr	Ala	His Phe	Ser Lys	Lys	Gly Glu	Glu
1280			1285			1290		
Glu Asn	Leu Glu	Gly Leu	Gly	Asn Gln	Thr Lys	Gln	Ile Val	Glu
1295			1300			1305		
Lys Tyr	Ala Cys	Thr Thr	Arg	Ile Ser	Pro Asn	Thr	Ser Gln	Gln
1310			1315			1320		
Asn Phe	Val Thr	Gln Arg	Ser	Lys Arg	Ala Leu	Lys	Gln Phe	Arg
1325			1330			1335		
Leu Pro	Leu Glu	Glu Thr	Glu	Leu Glu	Lys Arg	Ile	Ile Val	Asp
1340			1345			1350		
Asp Thr	Ser Thr	Gln Trp	Ser	Lys Asn	Met Lys	His	Leu Thr	Pro
1355			1360			1365		
Ser Thr	Leu Thr	Gln Ile	Asp	Tyr Asn	Glu Lys	Glu	Lys Gly	Ala
1370			1375			1380		
Ile Thr	Gln Ser	Pro Leu	Ser	Asp Cys	Leu Thr	Arg	Ser His	Ser
1385			1390			1395		
Ile Pro	Gln Ala	Asn Arg	Ser	Pro Leu	Pro Ile	Ala	Lys Val	Ser
1400			1405			1410		
Ser Phe	Pro Ser	Ile Arg	Pro	Ile Tyr	Leu Thr	Arg	Val Leu	Phe
1415			1420			1425		
Gln Asp	Asn Ser	Ser His	Leu	Pro Ala	Ala Ser	Tyr	Arg Lys	Lys
1430			1435			1440		
Asp Ser	Gly Val	Gln Glu	Ser	Ser His	Phe Leu	Gln	Gly Ala	Lys

1445	1450	1455
Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly 1460 1465 1470		
Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser 1475 1480 1485		
Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp 1490 1495 1500		
Leu Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His 1505 1510 1515		
Ile Tyr Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser 1520 1525 1530		
Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr 1535 1540 1545		
Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val 1550 1555 1560		
Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser 1565 1570 1575		
Lys Leu Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln 1580 1585 1590		
Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys 1595 1600 1605		
Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys 1610 1615 1620		
Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys 1625 1630 1635		
Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg 1640 1645 1650		
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu 1655 1660 1665		
Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr 1670 1675 1680		
Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile 1685 1690 1695		
Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys 1700 1705 1710		
Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr 1715 1720 1725		
Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser 1730 1735 1740		
Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr 1745 1750 1755		

Asp Gly 1760	Ser Phe Thr Gln Pro 1765	Leu Tyr Arg Gly Glu 1770	Leu Asn Glu
His Leu 1775	Gly Leu Leu Gly Pro 1780	Tyr Ile Arg Ala Glu 1785	Val Glu Asp
Asn Ile 1790	Met Val Thr Phe Arg 1795	Asn Gln Ala Ser Arg 1800	Pro Tyr Ser
Phe Tyr 1805	Ser Ser Leu Ile Ser 1810	Tyr Glu Glu Asp Gln 1815	Arg Gln Gly
Ala Glu 1820	Pro Arg Lys Asn Phe 1825	Val Lys Pro Asn Glu 1830	Thr Lys Thr
Tyr Phe 1835	Trp Lys Val Gln His 1840	His Met Ala Pro Thr 1845	Lys Asp Glu
Phe Asp 1850	Cys Lys Ala Trp Ala 1855	Tyr Phe Ser Asp Val 1860	Asp Leu Glu
Lys Asp 1865	Val His Ser Gly Leu 1870	Ile Gly Pro Leu Leu 1875	Val Cys His
Thr Asn 1880	Thr Leu Asn Pro Ala 1885	His Gly Arg Gln Val 1890	Thr Val Gln
Glu Phe 1895	Ala Leu Phe Phe Thr 1900	Ile Phe Asp Glu Thr 1905	Lys Ser Trp
Tyr Phe 1910	Thr Glu Asn Met Glu 1915	Arg Asn Cys Arg Ala 1920	Pro Cys Asn
Ile Gln 1925	Met Glu Asp Pro Thr 1930	Phe Lys Glu Asn Tyr 1935	Arg Phe His
Ala Ile 1940	Asn Gly Tyr Ile Met 1945	Asp Thr Leu Pro Gly 1950	Leu Val Met
Ala Gln 1955	Asp Gln Arg Ile Arg 1960	Trp Tyr Leu Leu Ser 1965	Met Gly Ser
Asn Glu 1970	Asn Ile His Ser Ile 1975	His Phe Ser Gly His 1980	Val Phe Thr
Val Arg 1985	Lys Lys Glu Glu Tyr 1990	Lys Met Ala Leu Tyr 1995	Asn Leu Tyr
Pro Gly 2000	Val Phe Glu Thr Val 2005	Glu Met Leu Pro Ser 2010	Lys Ala Gly
Ile Trp 2015	Arg Val Glu Cys Leu 2020	Ile Gly Glu His Leu 2025	His Ala Gly
Met Ser 2030	Thr Leu Phe Leu Val 2035	Tyr Ser Asn Lys Cys 2040	Gln Thr Pro
Leu Gly 2045	Met Ala Ser Gly His 2050	Ile Arg Asp Phe Gln 2055	Ile Thr Ala

Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His
 2060 2065 2070
 Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser
 2075 2080 2085
 Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile
 2090 2095 2100
 Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
 2105 2110 2115
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr
 2120 2125 2130
 Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn
 2135 2140 2145
 Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile
 2150 2155 2160
 Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg
 2165 2170 2175
 Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys
 2180 2185 2190
 Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln
 2195 2200 2205
 Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser
 2210 2215 2220
 Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp
 2225 2230 2235
 Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe
 2240 2245 2250
 Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys
 2255 2260 2265
 Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser
 2270 2275 2280
 Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys
 2285 2290 2295
 Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val
 2300 2305 2310
 Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His
 2315 2320 2325
 Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu
 2330 2335 2340
 Gly Cys Glu Ala Gln Asp Leu Tyr
 2345 2350

<210> 31

<211> 1471

<212> DNA

<213> Homo sapiens

<400> 31

```

atggcgcccg tcgccgtctg ggcgcgcgtg gccgtggac tggagctctg ggctcgggcg      60
cagcccttgc ccgccaggtt ggcatttaca cctacagccc cggagcccg gagcacatgc      120
cggtcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctcccgggcg      180
caacatgcaa aagtctcttg taccagacc tcggacaccg tgtgtgactc ctgtgaggac      240
agcacataca cccagctctg gaactgggtt ccgagtgctc tgagctgtgg ctcccgctgt      300
agctctgacc aggtggaaac tcaagcctgc actcgggaac agaaccgcat ctgcacctgc      360
aggcccgctt ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgcgccgctg      420
cgcaagtgcc gcccgggctt cgcgctggcc agaccaggaa ctgaacatc agacgtgggt      480
tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgacgg      540
ccccaccaga tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc      600
acgtccacgt cccccccg cgatgatggc ccaggggcag tacacttacc ccagccagtgc      660
tcacacagat ccaaacacac gcagccaact ccagaaccca gcactgtctc aagcacctcc      720
ttctgtctcc caatgggccc cagcccccca gctgaaggga gcactggcga ctctgcctct      780
ccagttggac tgatttgtgg tgtgacagcc ttgggtctac taataatagg agtggtgaa      840
tgtgtcatca tgaccaggt gaaaaagaag cccttgtgcc tgcagagaga agccaagggtg      900
cctcacttgc ctgccgataa ggcgcggggt acacagggcc ccgagcagca gcacctgctg      960
atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga      1020
agggcgccca ctccgaacca gccacaggca ccaggcgtgg agggccagtgg ggcgggggag      1080
gcccgggcca gcaccggag ctgagattct tcccctgggt gccatgggac ccaggccaat      1140
gtacactgca tcgtgaacgt ctgtagcagc tctgaccaca gtcacagtgc ctctcccaa      1200
gccagctcca caatgggaga cacagattcc agccctcagg agtccccgaa ggacgagcag      1260
gtccctctct ccaaggagga atgtgccttt cggtoacagc tggagacgcc agagacctgt      1320
ctggggagca ccgaagagaa gccctgccc cttggagtgc ctgatgtgtg gatgaagccc      1380
agttaaccag gccggtgtgg gctgtgtcgt agccaagtg ggctgagccc tggcaggatg      1440
acctgcgaa ggggcccgtg tccttcagg c

```

1471

<210> 32

<211> 461

<212> PRT

<213> Homo sapiens

<400> 32

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Leu
 1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser

	325		330		335	
Ala Leu Asp	Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly					
	340		345		350	
Val Glu Ala	Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser					
	355		360		365	
Asp Ser Ser	Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile					
	370		375		380	
Val Asn Val	Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln					
	385		390		395	
Ala Ser Ser	Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro					
	405		410		415	
Lys Asp Glu	Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser					
	420		425		430	
Gln Leu Glu	Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro					
	435		440		445	
Leu Pro Leu	Gly Val Pro Asp Ala Gly Met Lys Pro Ser					
	450		455		460	

<210> 33
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 33
 tccacctgtc ccgcagcgc cggtcgcgc cctcctgccg cagccaccga gccgccgtct 60
 agcgcgccga cctgcgcaco atgagagccc tgcggcgcg cctgcttctc tgcgtcctgg 120
 tcgtgagcga ctccaaaggc agcaatgaac ttcataaagt tccatcgaa cgtgactgtc 180
 taaatggagg aacatgtgtg tccaacaagt actctccaa cattcactgg tgcaactgcc 240
 caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300
 atggtcactt ttaccagga aagccagca ctgacaccat gggccggccc tgcctgccct 360
 ggaactctgc cactgtcctt cagcaaacgt accatgccca cagatctgat gctcttcagc 420
 tgggcctggg gaaacataat tactgcagga acccagacaa ccggaggcga cctgggtgct 480
 atgtgcaggt gggcctaaag cgccttgctc aagagtgcat ggtgcatgac tgcgcagatg 540
 gaaaaaagcc ctctctctct ccagaagaat taaaatttca gtgtggccaa aagactctga 600
 gggcccgctt taagattatt gggggagaat tcaccaccat cgagaaccag cctgggtttg 660
 cggccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca 720
 tcagcccttg ctgggtgatc agcgcacac actgcttcat tgattacca aagaaggagg 780
 actacatcgt ctacctgggt cgtcacaagg ttaactccaa cagcaaggg gagatgaagt 840
 ttgaggtgga aaacctcacc ctacacaagg actacagcgc tgacacgctt gctcaccaca 900

acgacattgc cttgtgtaag atcogttcca aggagggcag gtgtgcgcag ccatacccgga 960
 ctatacagac catctgcctg ccctcgatgt ataacgatcc ccagtttggc acaagctgtg 1020
 agatcactgg ctttggaataa gagaattota ccgactatct ctatccggag cagctgaaga 1080
 tgactgttgt gaagctgatt tcccaccggg agtgtcagca gcccactac tacggctctg 1140
 aagtcaccac caaatgctg tgtgtgtgtg accacagtg gaaaacagat tcttgccagg 1200
 gagactcagg gggaccctc gctgtgtccc tccaaggccg catgactttg actggaattg 1260
 tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac 1320
 acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggg 1380
 cccaggggag gaaacgggca ccaccgctt tcttgtgtgt tgtcattttt gcagtagagt 1440
 catctccatc agctgtaaga agagactggg aagat 1475

<210> 34
 <211> 431
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
 1 5 10 15
 Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
 20 25 30
 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
 35 40 45
 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
 50 55 60
 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
 65 70 75 80
 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
 85 90 95
 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp

	180		185		190
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val					
195		200		205	
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His					
210		215		220	
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly					
225		230		235	240
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val					
	245		250		255
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His					
	260		265		270
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys					
	275		280		285
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr					
	290		295		300
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys					
305		310		315	320
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val					
	325		330		335
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly					
	340		345		350
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys					
	355		360		365
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu					
	370		375		380
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys					
385		390		395	400
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu					
	405		410		415
Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu					
	420		425		430
<210> 35					
<211> 107					
<212> PRT					
<213> Mus musculus					
<400> 35					
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly					
1	5		10		15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala					
	20		25		30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile					
	35		40		45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 36
<211> 120
<212> PRT
<213> Mus musculus

<400> 36
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 37
<211> 120
<212> PRT
<213> Mus musculus

<400> 37
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120
 <210> 38
 <211> 106
 <212> PRT
 <213> Mus musculus
 <400> 38
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 39
 <211> 1039
 <212> DNA
 <213> Homo sapiens
 <400> 39
 tcctgcacag gcagtgccct gaagtgcctc ttcagagacc tttcttcata gactactttt 60
 tttttcttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120
 cattctcgtc atctctgagg acatcaccat catctcagga tgagggggcat gaagctgctg 180
 ggggcgctgc tggcactggc ggcctactg cagggggccg tgtccctgaa gatcgagcc 240
 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccacctcgt cagctacatt 300
 gtgcagatcc tgagccgcta tgacatcgcc ctgggtccagg aggtcagaga cagccacctg 360
 actgcctgtg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420
 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480

cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg 540
 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctccgggtt cacagaggtc, 600
 agggagtttg ccaattgttc cctgcatgcg gccccggggg acgcagtagc cgagatcgac 660
 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg 720
 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc 780
 ctgtggacaa gcccaccctt ccagtggctg atccccgaca gcgctgacac cacagctaca 840
 cccagccact gtgcctatga caggatcgctg gttgcaggga tgctgctcgg aggcgcggtt 900
 gttcccgact cggctcttcc cttaacttc caggctgcct atggcctgag tgaccaactg 960
 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgcgc agccccctcc 1020
 cacaccagtt gaactgcag 1039

<210> 40

<211> 282

<212> PRT

<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys
275 280

<210> 41
<211> 678
<212> DNA
<213> Mus musculus

<400> 41
gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60
ttctcttcca gggccagtc gttcgttggc tcaagcatcc actggtatca gcaagaaca 120
aatggtcttc caagccttct cataaagtat gttcttgagt ctatgtctgg gatcccttc 180
aggtttagtg gcagtggtgc agggacagat tttactctta gcatcaaac tgtggagtct 240
gaagatattg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggtctg 300
gggacaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa 360
cctggaggat coactgaaact ctctgtgttt gcctctggat tcatittcag taacctctgg 420
atgaactggg tccgccagtc tccagagaag gggottgagt gggtttgtga aattagatca 480
aaatctatta attctgcaac acattatgcg gagtctgtga aaggagggtt caccatctca 540
agagatgatt ccaaaagtgc tgtctacctg caaatgaccg acttaagaac tgaagacact 600
ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggc 660
accactctca cagtctcc 678

<210> 42
<211> 226
<212> PRT
<213> Mus musculus

<400> 42
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
 35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
 65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
 85 90 95

Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu
 100 105 110

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser
 115 120 125

Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val
 130 135 140

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser
 145 150 155 160

Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg
 165 170 175

Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met
 180 185 190

Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn
 195 200 205

Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
 210 215 220

Val Ser
 225

<210> 43
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 43
 gctgcatcag aagaggccat caagcacatc actgtccctc tgccatggcc ctgtggatgc 60
 gccctctgcc cctgctggcg ctgctggccc tctggggacc tgacccagcc gcagccttgy 120
 tgaaccaaca cctgtggcgc toacacctgg tggaagetct ctacctagtg tgcgggggaa 180
 gaggtcttct ctacacaccc aagaccgccg gggaggcaga ggacctgcag gtggggcgag 240
 tggagctggg cggggggccct ggtgcaggca gccctgcagcc cttggccctg gaggggtccc 300
 tgcagaagcg ttgcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg 360
 agaactactg caactagacg cagcccgcag gcagccccc acccgccgcc tctgtcaccc 420
 agagagatgg aataaagccc ttgaaccagc 450

<210> 44
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
 1 5 10 15
 Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
 20 25 30
 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
 35 40 45
 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
 50 55 60
 Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
 65 70 75 80
 Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
 85 90 95
 Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
 100 105 110

<210> 45
 <211> 1203
 <212> DNA
 <213> Hepatitis B virus

<400> 45
 atgggagggtt ggtcttccaa acctcgacaa ggcattggga cgaatcttct tgttccaat 60
 cctctgggat tctttccoga tcaccagttg gacctcggt tcggagccaa ctcaacaat 120
 ccagattggg acttcaacc caacaaggat cactggccag aggcaatcaa ggtaggagcg 180
 ggagacttcg ggccagggtt caccaccca caccggcgtc ttttgggtg gagccctcag 240
 gctcagggca tattgacaac agtgccagca gcgcctctc ctgtttccac caatcgagc 300
 tcaggaagac agcctactcc catctctcca cctctaagag acagtcatcc tcaggccatg 360
 cagtgaact ccacaacatt ccaccaagct ctgctagatc ccagagttag ggcctatat 420
 tttcctgctg gtggctccag ttccggaaca gttaaaccctg ttccgactac tgtctcacc 480
 atatcgtaaa tcttctcgag gactggggac cctgcacoga acatggagag cacaacatca 540
 ggattcttag gacctctgct cgtgttacag gcggggtttt tcttgttgac aagaatctc 600
 acaataccac agagtctaga ctggtggtg acttctctca attttctagg gggagcacc 660
 acgtgtcctg gccaaaattc gcagtcacca acctccaatc actcaccac ctctgtgct 720
 ccaatttgct ctggttatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac 780
 ctgctgctat gccctatctt cttgttggtt cttctggact accaaggtag gttgcccggt 840

tgtcctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt 900
 cctgctcaag gaacctctat gtttccctct tgggtgtgta caaaaccttc ggacggaac 960
 tgcacttgta ttcccatccc atcctctctgg gctttcgcaa gattcctatg ggagtgggcc 1020
 tcagtcggtt tctcctggct cagtttacta gtgcatttg ttcagtgggt cgcagggctt 1080
 tccccactg tttggcttcc agttatatgg atgatgtggt attgggggcc aagctctgac 1140
 aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt 1200
 tga 1203

<210> 46
 <211> 400
 <212> PRT
 <213> Hepatitis B virus

<400> 46
 Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
 1 5 10 15
 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30
 Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45
 Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60
 Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80
 Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95
 Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110
 Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125
 Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140
 Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160
 Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175
 Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190
 Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
 305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
 325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
 340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
 355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
 370 375 380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 385 390 395 400

<210> 47

<211> 799

<212> DNA

<213> Homo sapiens

<400> 47

cgaaccactc agggctcctgt ggacagctca cctagctgca atggctacag gctcccgac 60

gtccctgctc ctggcttttg gctgctctg cctgacctgg cttcaagagg gcagtgctt 120

cccaaccatt cccttatcca ggccttttga caacgctatg ctcgcgcgcc atcgtctgca 180

ccagctggcc tttagacctt accaggagtt tgaagaagcc tatatccaa aggaacagaa 240

gtattcatct ctgcagaacc ccagacctc cctctgtttc tcagagtcta ttccgacacc 300

ctccaacagg gaggaaacac aacagaaatc caacctagag ctgctccgca tctcctgct 360

gctcatccag tcgtggctgg agcccgctga gttcctcagg agtgccttcg ccaacagcct 420

ggtgtacggc gctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat 480

ccaaacgctg atggggaggc tggaagatgg cagcccccg actgggcaga tcttcaagca 540

gacctacagc aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg 600

gctgctctac tgcttcagga aggacatgga caaggtcgag acattcctgc gcagtgtgca 660

gtgccgctct gtggagggca gctgtggctt ctatgtgccc ggggtggcatc cctgtgaccc 720
 ctcccagtg cctctcctgg ccttggaagt tgccactcca gtgcccacca gccctgtcct 780
 aataaaatta agttgcatc 799

<210> 48
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
 1 5 10 15
 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
 20 25 30
 Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
 35 40 45
 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
 50 55 60
 Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
 65 70 75 80
 Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
 85 90 95
 Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
 100 105 110
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
 115 120 125
 Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
 130 135 140
 Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
 145 150 155 160
 Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
 165 170 175
 His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
 180 185 190
 Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
 195 200 205
 Arg Ser Val Glu Gly Ser Cys Gly Phe
 210 215

<210> 49
 <211> 963
 <212> DNA
 <213> Homo sapiens

<400> 49

atggagacag acacactcct gttatgggtg ctgctgtctt gggttccagg ttccactggt 60
gacgtcaggc gagggcccg gagcctgcgg ggcaggggacg cgcacagccc caccgccctgc 120
gtcccggcgg agtgcttcga cctgctgtgc cgcactgcgg tggcctgcgg gctcctgcgc 180
acgcccgccg cgaacccggc cggggccagc agccctgcgc ccaggacggc gctgcagccg 240
caggagtccg tgggcgcggg ggccggcgag gcggcggtcg acaaaactca cacatgccca 300
ccgtgcccg caccctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 360
aaggaccccc tcattgatctc ccggaccctt gaggtcacat gcgtggtggt ggacgtgagc 420
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 480
aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 540
gtcctgcacc aggactggct gaattggcaag gactacaagt gcaaggtctc caacaaagcc 600
ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 660
gtgtacaccc tgcgcccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 720
ctgggtcaaag gctttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 780
gagaacaact acaagaccac gcctcccgtg ttggactccg acggctcctt cttcctctac 840
agcaagctca ccgtggacaa gagcagggtg cagcagggga acgtctcttc atgtccgtg 900
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tcccgggaaa 960
tga 963

<210> 50

<211> 320

<212> PRT

<213> Homo sapiens

<400> 50

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg
20 25 30

Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
35 40 45

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
50 55 60

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
65 70 75 80

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
85 90 95

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
100 105 110

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 115 120
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 130 135 140
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 145 150 155 160
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 165 170 175
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 180 185 190
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 195 200 205
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 210 215 220
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 225 230 235 240
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 245 250 255
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 260 265 270
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 275 280 285
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 290 295 300
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 305 310 315 320
 <210> 51
 <211> 107
 <212> FRT
 <213> Homo sapiens
 <400> 51
 Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp

85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
 100 105
 <210> 52
 <211> 107
 <212> PRT
 <213> Mus musculus
 <400> 52
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105
 <210> 53
 <211> 119
 <212> PRT
 <213> Homo sapiens
 <400> 53
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30
 Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 54
 <211> 119
 <212> PRT
 <213> Mus musculus

<400> 54
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr
 1 5 10 15
 Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30
 Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ala
 115

<210> 55
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 55
 Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210
 <210> 56
 <211> 448
 <212> PRT
 <213> Homo sapiens
 <400> 56
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30
 Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

195 200 205
 Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445
 <210> 57
 <211> 8540
 <212> DNA
 <213> Homo sapiens
 <400> 57
 gacgtcgcgg ccgctctagg cctccaaaa agcctcctca ctactctctg aatagctcag 60
 aggcgagggc ggccctgcggc tctgcataaa taaaaaaaa tagtcagcca tgcatggggc 120
 ggagaatggg cggaactggg cggagttagg ggcgggatgg gcggagttag ggcggggact 180
 atggttgctg actaattgag atgcatgctt tgcatacttc tgcctgctgg ggagcctggg 240

gactttccac acctggttgc tgactaatg agatgcattc tttgcatact tctgcctget 300
 ggggagcctg gggactttcc acaccctaac tgacacacat tccacagaat taattccoct 360
 agttattaat agtaatacat tacgggggtca ttagttcata gcccatatat ggagttccgc 420
 gttacataac ttacggtaaa tggcccgctt ggctgaccgc ccaacgaccc ccgcccattg 480
 acgtcaataa tgacgtatgt tcccatagta acgccaatag ggactttcca ttgacgtcaa 540
 tgggtggact atttacggta aactgcccac ttggcagtac atcaagtgtg tcatatgcc 600
 agtacgcccc ctattgacgt caatgacggt aaatggcccg cctggcatta tgcccagtac 660
 atgaccttat gggactttcc tacttggcag tacatctacg tattagtcac gcctattacc 720
 atggtgatgc ggttttggca gtacatcaat gggcgtggat agcggtttga ctacacggga 780
 ttccaagtc tccaccccat tgacgtcaat gggagtgtgt tttggcacca aaataaacgg 840
 gactttccaa aatgtcgtaa caactccgcc ccattgacgc aaatgggcgg taggcgtgta 900
 cgggtgggag tctatataag cagagctggg tacgtgaacc gtcagatcgc ctggagacgc 960
 catcacagat ctctcaacct gagggcccc gctcagctcc tggggctctc gctgctctgg 1020
 ctcccagggt cagcatgtga tggtaacca gtggaaatca aacgtacggt ggctgcacca 1080
 tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 1140
 tgcctgctga ataaactcta tcccagagag gccaaagta agtgggaagg ggataacgcc 1200
 ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 1260
 agcctcagca gcacctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 1320
 tgcgaagtc ccatcagggt cctgagctcg ccctgcacaa agagcttcaa caggggagag 1380
 tgttgaattc agatccgtta acggttacca actacotaga ctggattcgt gacaacatgc 1440
 ggcgtgata tctactgatg atcagcctcg actgtgcctt ctagtgtcca gccatctgtt 1500
 gtttgcctct ccccgctgcc ttccttgacc ctggaagggt ccaactccac tgtcctttcc 1560
 taataaaatg aggaaaattg atgcatttgt ctgagttagt gtcattctat tctgggggggt 1620
 ggggtggggc aggcagacaa gggggaggat tgggaagaca atagcaggca tgcgtgggat 1680
 gcggtgggct ctatggaacc agctggggct cgacagctat gccaaagta cccctattg 1740
 acgtcaatga cggtaaatgg cccgcctggc attatgccca gtacatgacc ttatgggact 1800
 ttctactctg gcagtaacac tacgtattag tcatcgctat taccatggtg atgcggtttt 1860
 ggcagtacat caatggggct ggatagcgtt ttgactcacg gggatttcca agtctccacc 1920
 ccattgacgt caatggggat ttgttttggc accaaaatca acgggacttt ccaaaatgtc 1980
 gtaacaactc gcggccattg acgcaaatgg gcggtagggc tgtacggtgg gaggtctata 2040
 taagcagagc tgggtacgtc ctacatttca gtgatcagca ctgaacacag acccgtcgac 2100

atgggttgga gctcatctt gctcttctt gtcgtgttg ctacgcgtgt cgctagcacc 2160
 aaggggcccat cggtctctccc cctggcacc cctccaaga gcacctctgg gggcacacgc 2220
 gcctctgggt gctctgtcaa ggactacttc cccgaacgg tgacgggtgc gtggaactca 2280
 ggcgccctga ccagcgcggt gcacaccttc ccggtgtcc tacagtcctc aggactctac 2340
 tcctctagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 2400
 aacgtgaatc acaagcccg caacaccaag gtggacaaga aagcagagcc aaaaacttgt 2460
 gacaaaactc acaatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 2520
 ttctctctcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggctaca 2580
 tgcgtggtgg tggcagctgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 2640
 ggcggtgagg tgcataatgc caagacaaag ccgcggtgagg agcagtacaa cagcacgtac 2700
 cgtgtgtgca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggactacaag 2760
 tgcaaggctc ccaacaaagc cctcccagcc cccatcgaga aaacatctc caaagccaaa 2820
 gggcagcccc gagaaccaca ggtgtacacc ctgccccat ccgggagta gctgaccagg 2880
 aaccaggtea gctgacctg cctggtcaaa ggcttctat ccagcgacat gcgcgtggag 2940
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccg gctggactcc 3000
 gacggctctc ttctctctc cagcaagctc accgtggaca agagcagtg gcagcagggg 3060
 aacgtctct catgctcgt gatgcatgag gctctgcaca accactacac gcagaagagc 3120
 ctctccctgt ctccgggtaa atgaggatcc gttaacggt accaactacc tagactggat 3180
 tcgtgacaac atgcggcggt gatctctac tatgatcac ctgcactgtg ccttctagt 3240
 gccagccatc tgttgtttgc cctcccccg tgccttctt gacctggaa ggtgccactc 3300
 ccactgtctt ttctcaataa aatgaggaaa ttgcatogca ttgtctgagt aggtgtcatt 3360
 ctattctggg ggtgtgggtg gggcaggaca gcaaggggga ggattgggaa gacaatagca 3420
 ggcatctggt ggatcggtg ggctctatgg aaccagctgg ggctcgacag cgtcggtatc 3480
 cccgatcccc agctttgctt ctcaatttct tatttgcata atgagaaaaa aaggaatt 3540
 aattttaaca ccaattcagt agttgattga gcaaatcggt tgccaaaaag gatgcttag 3600
 agacagtgtt ctctgcacag ataaggacaa acattattca gaggagtag ccagagctga 3660
 gactcctaag ccagtgtgtg gcacagcatt ctaggagaa atatgttgt catcaccgaa 3720
 gctgtattcc gttagagcac accttggtaa gggccaatct gctcacacag gatagagagg 3780
 gcaggagcca gggcagagca tataaggtga ggtaggatca gttgctctc acatttgcct 3840
 ctgacatagt tgtgttggga gcttgatag cttggacagc tcagggctgc gatttcgcgc 3900

caaacttgac ggcaatccta gcgtgaagcg tggtaggatt ttatccccgc tgccatcatg 3960
 gttcgaccat tgaactgcac cgtgcgcgtg tccaaaaata tggggatttg caagaacgga 4020
 gacctaccct ggccctcgct caggaacgag ttcaagtact tccaaagaat gaccacaacc 4080
 tcttcagtgg aaggtaaaca gaatctgggt attatgggta ggaaaacctg gttctccatt 4140
 cotgagaaca atcgaccttt aaaggacaga attaatatag ttctcagtag agaactcaaa 4200
 gaaccaccac gaggagctca ttttcttgcc aaaagtttg atgatgcctt aagacttatt 4260
 gaacaaccgg aattggcaag taaagtagac atggtttgga tagtcggagg cagttctggt 4320
 taccaggaag coactgaatca accagggcac cttagactct ttgtgacaag gatcatgcag 4380
 gaatttgaaa gtgacacgtt tttccagaa attgatttg ggaaatataa acttctccca 4440
 gaatcccgag gcgtctcttc tgaggctcac gagggaaaag gcatcaagta taagtgtgaa 4500
 gtctacgaga agaaagacta acagggaagat gctttcaagt tctctgctcc cctcctaaag 4560
 tcatgcattt ttataagacc atgggacttt tgctggcttt agatcagcct cgactgtgcc 4620
 ttctagttag cagccatctg ttgtttgccc ctccccctg ccttccctga cctcggaagg 4680
 tgccactccc actgtccttt cctaataaaa tgaggaaatt gcatcgcatg gtctgagtag 4740
 gtgtcattct attctggggg gtggggtggg gcaggacagc aagggggagg attgggaaga 4800
 caatagcagg catgctgggg atgcggtggg ctctatggaa ccagctgggg ctgcagctac 4860
 tagctttgct tctcaatttc ttatttgcat aatgagaaaa aaaggaaaat taattttaac 4920
 accaattcag tagttgattg agcaaatgcg ttgcaaaaaa ggatgcttta gagacagtgt 4980
 tctctgcaca gataaggaca aacattatct agaggggagta cccagagctg agactcctaa 5040
 gccagtgagt ggcacagcat tctagggaga aatatgcttg tcatcaccga agcctgattc 5100
 cgtagagcca cacttggtga agggccaatc tgctcacaca ggatagagag ggcaggagcc 5160
 agggcgagagc atataagggt aggtaggatc agttgctcct cacatttgct tctgacatag 5220
 ttgtgttggt agcttggtgc gatcctctat ggttgaacaa gatggattgc acgcagggtc 5280
 tcggcgctg ttgggtggaga ggctattcgg ctatgactgg gcacaacaga caatcggtg 5340
 ctctgatgcc gcggtgttcc ggctgtcagc gcaggggcgc ccggttcttt ttgtcaagac 5400
 cgacctgtcc ggtgccctga atgaactgca ggacgaggca gcgcggctat cgtggtgtggc 5460
 cagcaggggc gttccttgcg cagctgtgct cgacgttgct actgaagcgg gaagggaactg 5520
 gctgctattg ggogaagtgc cggggcagga tctcctgtca tctcactctg ctctcgccga 5580
 gaaagtatcc atcatggctg atgcaatgcg gcggtgcat acgcttgatc cggtcacctg 5640
 cccattcgac caccaagcga aacatcgcat cgagcgagca cgtactcgga tggaaagcgg 5700
 tcttgctgat caggatgac ttggacgaaga gcatcagggg ctgcgcgcag ccgaactggt 5760

cgccaggctc aaggcgcgca tgcccagcgg cgaggatctc gtcgtgaccc atggcgatgc 5820
 ctgcttgccg aatatcatgg tggaaaatgg ccgcttttct ggattcatcg actgtggccg 5880
 gctgggtgtg gcggaccgct atcaggacat agcgttggct acccgtgata ttgctgaaga 5940
 gcttgccggc gaatgggctg accgcttctc cgtgctttac ggtatcgccg ctctcccgatt 6000
 cgcagcgcat cgccttctat cgccttcttg acgagttctt ctgagcggga ctctgggggt 6060
 cgaaatgacc gaocaagcga cgcccaacct gccatcacga gatttcgatt ccacgcgcgc 6120
 cttctatgaa aggttgggct tcggaatcgt ttcccgggac gccggctgga tgatctcca 6180
 gcgcggggat ctcatgtcgg agttcttcgc ccacccaac ttgtttattg cagcttataa 6240
 tgggttcaaaa taaagcaata gcatacaaaa ttacacaaat aaagcatttt ttctactgca 6300
 ttctagtgtg ggtttgtcca aactcatcaa tctatcttat catgtctgga tcgcgccgcg 6360
 gatcccgctg agagcttgcc gtaatcatgg tcatagctgt ttccgtgtg aaattgttat 6420
 ccgctcacia ttocacacia catacgagcc ggagcataaa gtgtaagcc tggggtgcct 6480
 aatgagttag ctaactcaca ttaattgcgt tgcgctcact gcccgcttcc cagtcgggaa 6540
 acctgctgtg ccagctgcac taatgaatcg gccaacgcgc ggggagaggg ggtttgcgta 6600
 ttggcgctcc ttccgcttcc tcgctcactg actcgtcgcg ctccgctcgtt cggctcgccg 6660
 gagcggtatc agctcactca aaggcggtaa tacggttata cacagaatca ggggataaog 6720
 caggaaagaa catgtgagca aaaggccagc aaaaggccag gaacogtaaa aaggccgcgt 6780
 tgctggcggt ttcccatagc ctccgcccc ctgacgagca tcacaaaaat cgacgctcaa 6840
 gtcagaggtg gcgaaacccg acaggactat aaagatacca ggcgtttccc cctggaagct 6900
 cctcgtgctg ctctcctgtt ccgacctgc cgttacccg atacctgtcc gcctttctcc 6960
 cttcggaag cgtggcgctt tctcaatgct cagcgttag gtatctcagt tcggtgtagg 7020
 tegtctgctc caagctgggc tgtgtgcacg aaaccccgct tcagcccgac cgctgcgct 7080
 tatccggtaa ctatcgtctt gagtccaacc cggtaagaca cgacttatcg ccactggcag 7140
 cagccactgg taacaggatt agcagagcga ggtatgtagg cgggtctaca gagtcttga 7200
 agtgggtggc taactacggc tactactagaa ggacagtatt tgggtatctg gctctgtgta 7260
 agccagttae cttcggaaaa agagttggta gctcttgatc cggcaaaaca accacgcgtg 7320
 gtagcgggtg tttttttgtt tgcaagcagc agattacgcg cagaaaaaaa ggatctcaag 7380
 aagatccttt gatcttttct acggggctcg acgctcagtg gaacgaaaac tcacgttaag 7440
 ggatttttgt catgagatta tcaaaaagga tcttcacctg gatcctttta aattaaaaat 7500
 gaagttttta atcaatctaa agtatatatg agtaaacctg gctctgacagt taccaatgct 7560

taatcagtgga ggcacccatc tcagcgatct gtctatttcg ttcacccata gttgcctgac 7620
 tccccgtcgt gtagataact acgatacggg agggcctacc atctggcccc agtgctgcaa 7680
 tgataccgag agacccacgc tcacgggctc cagatttacc agcaataaac cagccagccg 7740
 gaaggccgga gcgcagaagt ggtcctgcaa ctttatccgc ctccatccag tctattaatt 7800
 gttgcgggga agctagagta agtagttcgc cagttaatag ttgcgcaac gttgttgcca 7860
 ttgtacacag catcgtgggt tcacgctcgt cgtttgggtt ggcttcattc agctccgggt 7920
 cccaacgac aaggcgagtt acatgatccc ccattgtgtg caaaaaagcg gttagctcct 7980
 tcggtcctcc gatcgttgct agaagtaagt tggccgcagt gttatcactc atggttatgg 8040
 cagcactgca taattctctt actgcatgc catccgtaag atgcttttct gtgactgggt 8100
 agtactcaac caagtcattc tgagaatagt gtatgcggcg accgagtgc tcttgcccg 8160
 cgtcaatacg ggataatacc gcgccacata gcagaacttt aaaagtgtc atcatggaa 8220
 aacgttcttc gggcgaaaa ctctcaagga tcttaccgct gttgagatcc agtctgatgt 8280
 aacccactcg tgcacccaac tgatcttcag catcttttac ttccaccagc gtttctgggt 8340
 gagcaaaaaa aggaagcgaa aatgcgcgaa aaaagggaaat aaggcgcgaca cggaaatgtt 8400
 gaatactcat actcttctt tttcaatatt attgaagcat ttatcagggt tattgtctca 8460
 tgagcggata catatttgaa tgtatttaga aaaataaaca aatagggggt ccgcgcacat 8520
 ttcccggaaa agtgccacct 8540

<210> 58

<211> 9209

<212> DNA

<213> Mus musculus

<400> 58

gacgtcggcg ccgctctagg cctccaaaaa agcctcctca ctacttctgg aatagctcag 60
 aggcgcaggc ggctcgggcc tctgcataaa taaaaaaat tagtcagcca tgcattgggc 120
 ggagaatggg cggaaactgg cgaggttagg ggcgggatgg gcggagttag gggcgggact 180
 atggttgctg actaattgag atgcatgctt tgcatacttc tgcctgctgg ggagcctggg 240
 gactttccac acctgggtgc tgactaattg agatgcattc ttgcatact tctgctgct 300
 ggggagcctg gggactttcc acaccctaac tgacacacat tccacagaat taattccct 360
 agttattaat agtaatoaat tacgggggtc ttagttcata gcccatatat ggagttccgc 420
 gttacataac ttacgggtaa tggcccgctt ggctgaccgc ccaacgaccc ccgccattg 480
 acgtcaataa tgacgtatgt tcccatagta acgccaatag ggactttcca ttgacgtcaa 540
 tgggtggact atttacggta aactgcccac ttggcagtag atcaagtgtg tcatatgcca 600
 agtacgcccc ctattgacgt caatgacggt aaatggcccg cctggcatta tgcccagtag 660

atgaccttat gggactttcc tacttggcag tacatctacg tattagtcat cgtattatcc 720
 atgggtgatgc ggttttggca gtacatcaat gggcgtggat accggtttga ctcaocggga 780
 ttccaagtc tccaccccat tgacgtcaat gggagtttgt tttggcacca aaatcaacgg 840
 gactttccaa aatgtcgtaa caactccgcc ccattgacgc aaatgggcgg taggcgtgta 900
 cgggtgggagg tctatataag cagagctggg tacgtgaacc gtcagatcgc ctggagacgc 960
 catcacagat ctctactat ggattttcag gtgcagatta tcagcttctc getaatcagt 1020
 gcttcagtca taatgtccag aggacaaatt gttctctccc agtctccage aatcctgtct 1080
 gcatctccag gggagaaggc cacaatgact tgcagggcca gctcaagtgt aagttacatc 1140
 cactggttcc agcagaagcc aggatctccc cccaaacctc ggatttatgc cacatccaac 1200
 ctggcttctg gagtccctgt tcgcttcagt ggcagtgggt ctgggacttc ttaactcttc 1260
 acaatcagca gagtggaggc tgaagatgct gccacttat actgccagca gtggactagt 1320
 aaccaccca cgttcggagg ggggaccaag ctggaaatca aacgtacggt ggctgcacca 1380
 tctgtcttca tcttccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 1440
 tgcctctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 1500
 ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 1560
 agcctcagca gcacctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 1620
 tgcgaagtca cccatcaggc cctgagctcg cccgtcaca agagcttcaa caggggagag 1680
 tgttgaattc agatccgta acggttacca actacctaga ctggattcgt gacaacatgc 1740
 ggccgtgata tctactatg atcagcctcg actgtgcctt ctagttgccca gccatctgtt 1800
 gtttgcctc ccccggtgc ttccttgacc ctggaagggt ccactccac tgtcctttcc 1860
 taataaaatg aggaatgtc atcgattgt ctgagtagg gtcattctat tctggggggt 1920
 ggggtggggc aggacagcaa gggggaggat tgggaagaca atagcaggca tgctggggat 1980
 gcggtgggct ctatggaacc agctggggct cgacagctat gccaaagtac ccccatattg 2040
 acgtcaatga cggtaaatg cccgcctggc attatgccca gtacatgacc ttatgggact 2100
 ttcactcttg gcagtcacac tacgtattag tcatcgctat taccatgggt atgcgggttt 2160
 ggcagtacat caatggcggt gगतagcggt ttgactcacg gggatttcca agtctccacc 2220
 ccattgacgt caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc 2280
 gtaacaaact cgccttcatt acgcaaatg gcggtaggcg tgtacgggtg gaggtctata 2340
 taagcagagc tgggtcagtc ctcacattca gtgatcagca ctgaacacag acccgtcgac 2400
 atgggttgga gcctcatctt gctcttcctt gtcgtgttg ctacgcgtgt cctgtccag 2460

gtacaactgc agcagcctgg ggcagagctg gtgaagcctg gggcctcagt gaagatgtcc 2520
 tgcaaggcct ctggctacac attaccagt tacaatatgc actgggtaaa acagacacct 2580
 ggtcggggcc tggaatggat tggagctatt tatccggaa atggtgatac ttctacaaat 2640
 cagaagtcca aaggcaaggc cacattgact gcagacaaat cctccagcac agcctacatg 2700
 cagctcagca gectgacatc tgaggactct gcggtctatt actgtgcaag atcgacttac 2760
 tacggcgggtg actggtactt caatgtctgg ggcgcaggga ccacggctac cgtctctgca 2820
 gctagcacca agggcccatc ggtctctccc ctggcaccct cctccaagag cacctctggg 2880
 ggcacagcgg cctggggtg cctggccaag gactacttcc cgaaccgggt gacgggtgtg 2940
 tggaactcag gcgcctgac cagcggcgtg cacaccttcc cggctgtcct acagtctcca 3000
 ggactctact cctccagcag cgtgggtgacc gtgcctcca gcagcttggg caccagacc 3060
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agcagagccc 3120
 aaatcttgtg acaaaactca cacatgccca ccgtgccagc cacctgaact cctgggggga 3180
 ccgtcagtct tctctctccc cccaaaacc aaggacacc tcatgatctc ccggaccct 3240
 gaggtcacat gcgtgggtgt ggacgtgagc caccgaagacc ctgagggtcaa gttcaactgg 3300
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 3360
 agcacgtacc gtgtggctcag cgtctcacc gtctgcacc aggactggct gaatggcaag 3420
 gagtacaagt goaaggctct caacaaagcc ctcccagccc ccacgcagaa aacctctcc 3480
 aaagccaaag ggcagccccg agaaccacag gtgtacacc tgccccatc ccgggatgag 3540
 ctgaccaaga accaggtcag cctgacctgc ctggtcaaa gcttctatcc cagcgacatc 3600
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 3660
 ctggactccg acggctcctt ctctctctac agcaagctca ccgtggacaa gagcagggtg 3720
 cagcagggga acgtctctct atgctcctg atgcatgagg ctctgcacaa ccaactacac 3780
 cagaagagcc tctcctgtc tccgggtaaa tgaggatccg ttaacggtta coaactacct 3840
 agactggatt cgtgacaaca tgccgcccgt atatctcagt atgatcagcc tcgactgtgc 3900
 cttctagttg ccagccatct gttgtttgcc cctccccgt gccttcttg accctggaag 3960
 gtgccactcc cactgtcctt tcttaataaa atgaggaaat tgcatcgcat tgtctgagta 4020
 ggtgtcattc tattotgggg ggtgggggtg ggcaggacag caagggggag gattgggaag 4080
 acaatagcag gcattgctgg gatgcgggtg gctctatgga accagctggg gctcgacagc 4140
 gctggatctc ccgatcccca gctttgcttc tcaatttctt atttgataa tgagaaaaa 4200
 aggaaaatta attttaaac caattcagta gttgattgag caaatgcgtt gccaaaaag 4260
 atgctttaga gacagtgtc tctgcacaga taaggacaaa cattattcag agggagtacc 4320

cagagctgag actcctaagc cagtgagtgg cacagcattc tagggagaaa tatgcttgtc 4380
 ataccgaag cctgattccg tagagccaca ccttggttaag ggccaatctg ctcacacagg 4440
 atagagaggg caggagccag ggcagagcat ataaggtgag gtaggatcag ttgctcctca 4500
 catttgcttc tgacatagtt gtgttgggag cttggatagc ttggacagct cagggtctgc 4560
 atttcgcgcc aaacttgacg gcaatccctag cgtgaaggct ggtaggattt tatcccgct 4620
 gccatcatgg ttogaccatt gaactgcacg gtogccgtgt cccaaaatat ggggattgac 4680
 aagaacggag acctaccctg gcctcgcctc aggaacgagt tcaagtactt ccaagaagt 4740
 accacaacct ctctagtgga aggtaaacag aatctggtga ttatgggtag gaaaacctgg 4800
 ttctccattc ctgagaagaa togacctta aaggacagaa ttaatatagt tctcagtaga 4860
 gaactcaaag aaccaccaag aggagctcat ttcttgcca aaagtgtgga tgatgcctta 4920
 agacttattg aacaacggga attggcaagt aaagtagaca tggtttggtt agtcggaggc 4980
 agttctgttt accaggaagc catgaatcaa ccaggccacc ttagactctt tgtgacaagg 5040
 atcatgcagg aatttgaag tgacacgttt tcccagaaa ttgatttggg gaaatataaa 5100
 ctctcccgag aatacccgag cgtcctctct gaggtccagg aggaaaaagg catcaagtat 5160
 aagtttgaag tctacgagaa gaaagactaa caggaaagtg ctttcaagtt ctctgctccc 5220
 ctctaaagc tatgcatttt tataagacca tgggactttt gctggcttta gatcagcctc 5280
 gactgtgcct tctagtggcc agccatctgt tgtttgcccc tccccgtgc ctctcctgac 5340
 cctggaaggt gccactccca ctgtcctttc ctaataaaat gaggaattg catgcattg 5400
 tctgagtagg tgtcattcta ttctgggggg tgggtgggg caggacagca agggggagga 5460
 ttgggaagac aatagcaggc atgctgggga tgcggtgggc tctatggaac cagctggggc 5520
 tcgagctact agcttgcct ctcaattctt tatttgcata atgagaaaaa aaggaaaatt 5580
 aattttaaca ccaattcagt agttgattga gcaaatcgt tgccaaaag gatgctttag 5640
 agacagtgtt ctctgcacag ataaggacaa acattattca gagggagtac ccagagctga 5700
 gactcctaag ccagtgagt gcacagcatt ctaggagaa atatgcttgt catcacgaa 5760
 gcctgattcc gtagagccac accttggtta gggccaatct gctcacacag gatagagagg 5820
 gcaggagcca gggcagagca tataaggtga ggtaggatca gttgctctc acatttgctt 5880
 ctgacatagt tgtgttggga gcttgatcg atcctctatg gttgaacaag atggattgca 5940
 cgcaggttct ccggccgctt ggtggagag gctattcggc tatgactggg cacaacagac 6000
 aatcgctgc tctgatgcc ccgtgttcg gctgtcagc cagggcgcc cggttctttt 6060
 tgtcaagacc gaactgtccg gtgcctgaa tgaactgcag gacgaggcag cgcggctatc 6120

gtggtctggcc acgacggggc ttccttgccg agctgtgctc gacgttgca ctgaagcggg 6180
 aagggaactgg ctgctattgg gcgaagtgcc ggggcaggat ctctgtcat ctccacttgc 6240
 tctgtccgag aaagtatcca tcatggctga tgcaatggcg cggtgcata cgcttgatcc 6300
 ggctacctgc ccatcgacc accaagcgaa acatcgctc gagcgagcac gtactcggat 6360
 ggaagccggt ctgtctgac aggatgatct ggacgaagag catcaggggc tcgcgccagc 6420
 cgaactgttc gccaggetca aggcgcgcat gcccgacggc gaggatctcg tcgtgaccca 6480
 tggcgatgcc tgcttgcga atatcatggt ggaaaatggc cgcttttctg gattoatcga 6540
 ctgtggcggc ctgggttggt cggaccgcta tcaggacata gcgttgcta cccgtgatat 6600
 tgctgaagag ctggcgggc aatgggtga ccgcttctc gtgctttacg gtatcgccgc 6660
 tcccgattcg cagcgcacg ccttctatcg cctcttgac gaggttctct gagcgggact 6720
 ctggggttgc aaatgaccga ccaagcgacg cccaacctgc catcacgaga ttctgattcc 6780
 accgcgcctc tctatgaaa gttgggcttc ggaatcgttt tcgggacgc cggtcggatg 6840
 atctccagc cgggggatct catgctggag ttcttcgcc accccaactt gtttattgca 6900
 gcttataatg gttacaaa aagcaatagc atcacaaatt tcacaaaata agcatTTTT 6960
 tcaactgatt ctagtgtgg tttgtccaaa ctcatcaato tatcttata tgctggatc 7020
 gcggcgcga tcccgctgag agcttgcgct aatcatggc atagctgttt cctgtgtgaa 7080
 attgttacc gctcacaatt ccacacaaca tacgagcgg aagcataaag tgtaaagcct 7140
 ggggtgccta atgagtgcg taactcacat taattgcgtt gcgctcaatg cccgcttcc 7200
 agtcgggaaa cctgtctgc cagctgcatt aatgaatcg ccaacgcgc gggagaggcg 7260
 gtttgctat tgggcgctct tcgcttctc cgctcactga ctgctgcgc tcgctgttc 7320
 ggctgcggc agcggtatca gctcactcaa aggcggtaat acggttacc acagaatcag 7380
 gggataacgc aggaagaac atgtgagcaa aaggccagca aaaggccagg aaccgtaaaa 7440
 aggcgcgctt gctggcgttt ttccataggc tcgcgcgcgc tgacgagcat caaaaaattc 7500
 gacgtcaag tcagaggtg cgaacccga caggactata aagataccag gcgtttcccc 7560
 ctggaagctc cctgtgcgc tctcctgttc cgaacctgc gcttacgga taactgtccg 7620
 cctttctccc ttggggaagc gtggcgcttt ctcaatgctc acgctgtagg tatctcagt 7680
 cgggttaggt cgttcgctcc aagctgggct gtgtgcacga acccccgctt cagcccgacc 7740
 gctgcgcctt atccggtaac tatgtcttg agtccaaccc ggtaagacac gacttatcgc 7800
 cactggcagc agccactggt aacaggatta gcagagcgag gtatgtaggc ggtgctacag 7860
 agttcttgaa gtggggcct aactacggct acactagaag gacagtattt ggtatctgcg 7920
 ctctgctgaa gccagttacc ttcggaaaaa gagttgtag ctcttgatcc ggcaacaaa 7980

ccaccgctgg tagcgggtgg ttttttgttt gcaagcagca gattacgcgc agaaaaaaag 8040
 gatctcaaga agatcccttg atcttttcta cggggctctga cgcctcagtg aacgaaaact 8100
 cacgttaagg gatttttggtc atgagattat caaaaaggat cttcacctag atccttttaa 8160
 attaaaaatg aagtttttaa tcaatctaaa gtatatatga gtaaacttgg tctgacagtt 8220
 accaatgctt aatcagtgag gcacctatct cagcgatctg tctatttcgt tcatccatag 8280
 ttgcctgact ccccgctgtg tagataacta cgatacggga gggcttacc a tctgcccaca 8340
 gtgctgcaat gataccgcga gaccacgcgt caccggctcc agatttatca gcaataaacc 8400
 agccagccgg aagggccgag cgcagaagtg gtcctgcaac tttatccgcc tccatccagt 8460
 ctattaattg ttgcgggaa gctagagtaa gtggttcgcc agttaatagt ttgcgcaacg 8520
 ttgttgccat tgctacagcg atcggtggtg cacgctcgtc gtttggtatg gcttcattca 8580
 gctccggttc ccaacgatca aggcgagtta catgatccc catgttggtg aaaaaagcgg 8640
 ttagctcctt cggctcctcg atcggttgca gaagtaagtt ggccgcagtg ttatcactca 8700
 tggttatggc agcactgcac aattctctta ctgtcatgcc atcogtaaga tgcttttctg 8760
 tgactggtga gtactcaacc aagtcattct gagaatagtg tatgcggcga ccgagttgct 8820
 cttgcccgcg gtcaatacgg gataatacgg cgcacatag cagaacttta aaagtgtca 8880
 tcattggaaa acgtttctcg gggcgaaaac tctcaaggat cttacogctg ttgagatcca 8940
 gttcgtatga acccactcgt gcaccaact gatcttcagc atcttttact ttcaccagcg 9000
 tttctgggtg agcaaaaaa ggaaggcaaa atgcgcgcaa aaaggggaata agggcgacac 9060
 ggaaatgttg aatactcata ctcttctctt ttcaatat taagaagcatt tatcagggtt 9120
 attgtctcat gagcggatac atatttgaat gtatttagaa aaataaaca atagggggtc 9180
 cggccacatt tcccgaaaa gtgccacct 9209

<210> 59
 <211> 384
 <212> DNA
 <213> Mus musculus

<400> 59
 atggatttct aggtgcagat tatcagcttc ctgctaata ctgcttcagt cataatgtcc 60
 agaggcgaaa ttgttctctc ccagttctca gcaatcctgt ctgcatctcc aggggagaag 120
 gtcacaaatg cttgcaggcg cagctcaagt gtaagttaca tccactggtt ccagcagaag 180
 ccaggatcct ccccaaaacc ctggatttat gccacatcca acctggcttc tggagtccct 240
 gttcgcttca gtggcagtg gtctgggact tcttactctc tcacaatcag cagagtgagg 300
 gctgaagatg ctgccactta ttactgccag cagtggacta gtaaccacc caggttcgga 360

ggggggacca agctggaaat caaa

384

<210> 60
 <211> 128
 <212> PRT
 <213> Mus musculus

<400> 60
 Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 115 120 125

<210> 61
 <211> 420
 <212> DNA
 <213> Mus musculus

<400> 61
 atgggttgga gcctcatctt gctcttccctt gtcgtgtgtg ctacgcgtgt cctgtcccag 60
 gtacaactgc agcagcctgg ggctgagctg gtgaagcctg gggcctcagt gaagatgtcc 120
 tgcaaggctt ctggctacac atttaccagt tacaatatgc actgggtaaa acagacacct 180
 ggtcggggcc tgggaatgat tggagctatt tatcccgaa atggtgatac ttctactaat 240
 cagaagtta aaggcaaggc cacattgact gcagacaaat cctccagcac agcctacatg 300
 cagctcagca gcctgacatc tgaggactct gcggtctatt actgtgcaag atcgacttac 360
 tacggcgtg actggtactt caatgtotgg gggcgaggga ccacggtcac cgtctctgca 420

<210> 62
 <211> 140
 <212> PRT
 <213> Mus musculus

<400> 62
 Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
 50 55 60

Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
 115 120 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
 130 135 140

<210> 63
 <211> 1395

<212> DNA

<213> Homo sapiens

<400> 63
 atgtattcca atgtgatagg aactgtaacc tctggaaaaa ggaagggttta tcttttgtcc 60
 ttgctgctca ttgctttctg ggactgcgtg acctgtcaag ggagccctgt ggacatctgc 120
 acagccaagc cgcgggacat tcccatgaat cccatgtgca ttacccgtc ccgggagaag 180
 aaggcaactg aggatgaggg ctccagaacag aagatcccgagg gccaccaaa ccggcggtgc 240
 tgggaactgt ccaaggccaa ttcccgcttt gctaccactt tctatcagca cctggcagat 300
 tccaagaatg acaatgataa cattttctctg tcaccctctga gtatctccac ggcctttgtct 360
 atgaccaagc tgggtgcctg taatgacacc ctccagcaac tgatggagggt atttaagttt 420
 gacaccatat ctgagaaaac atctgatcag atccacttct tctttgccaa actgaactgc 480
 cgactctatc gaaaagccaa caaatctctc aagttagtat cagccaatcg cctttttgga 540
 gacaaatccc ttaccttoaa tgagacctac caggacatca gtgagttggt atatggagcc 600
 aagctccagc ccctggactt caaggaaaaa gcagagcaat ccagagcggc catcaacaaa 660
 tgggtgttcaa ataagacaga aggcggaatc accgatgtca ttccctcgga agccatcaat 720
 gagctcactg tcttggtgct ggttaacacc atttacttca agggcctgtg gaagtcaaaag 780
 ttccgcctgt agaacaag gaagggaactg ttctacaagg ctgatggaga gtcgtgttca 840
 gcatctatga tgtaccagga aggcgaagttc cgttatcggc cgttggtgtga aggcacccag 900

gtgcttgagt tgcccttcaa aggtgatgac atcaccatgg tcctcatctt gcccaagcct 960
 gagaagagcc tggccaaggt ggagaaggaa ctcacccag aggtgctgca ggagtggctg 1020
 gatgaattgg aggagatgat gctggtggtc cacatgcccc gcttccgcat tgaggacggc 1080
 ttcagtttga aggagcagct gcaagacatg ggccttgctg atctgttcag cccgtgaaaag 1140
 tccaaactoc caggatattgt tgcagaaggc cgagatgacc tctatgtctc agatgcattc 1200
 cataaggcat ttcttgaggt aaatgaagaa ggcagtgaag cagctgcaag taccgctgtt 1260
 gtgattgctg gccgttgct aaacccaac agggtgactt tcaaggccaa caggcccttc 1320
 ctggttttta taagagaagt tcctctgaac actattatct tcatgggcag agtagccaac 1380
 ccttggttta agtaa 1395

<210> 64

<211> 464

<212> PRT

<213> Homo sapiens

<400> 64

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val
 1 5 10 15

Tyr Leu Leu Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys
 20 25 30

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 35 40 45

Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
 50 55 60

Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
 65 70 75 80

Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
 85 90 95

His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
 100 105 110

Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
 115 120 125

Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
 130 135 140

Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
 145 150 155 160

Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
 165 170 175

Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
 180 185 190

Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys

195										200										205										
Glu	Asn	Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn															
210						215					220																			
Lys	Thr	Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn															
225					230					235					240															
Glu	Leu	Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu															
				245					250					255																
Trp	Lys	Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr															
		260						265					270																	
Lys	Ala	Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly															
	275						280					285																		
Lys	Phe	Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu															
	290					295					300																			
Pro	Phe	Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro															
305				310					315					320																
Glu	Lys	Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu															
			325					330					335																	
Gln	Glu	Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met															
			340					345					350																	
Pro	Arg	Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln															
	355					360					365																			
Asp	Met	Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro															
	370					375					380																			
Gly	Ile	Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe															
385					390					395				400																
His	Lys	Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala															
			405					410					415																	
Ser	Thr	Ala	Val	Val	Ile	Ala	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val															
			420					425					430																	
Thr	Phe	Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro															
	435					440					445																			
Leu	Asn	Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys															
	450					455					460																			

<210> 65

<211> 1962

<212> DNA

<213> Homo sapiens

<400> 65

atgcgtcccc tgcgcccccg cgccgcgctg ctggcgctcc tggcctcgct cctggccgcg 6

cccccggtgg ccccgccgca ggcgccgcac ctggtgcagg tggacgcggc ccgcgcgctg 12

tggccctctgc ggcgttctgc gaggagcaca ggcttctgcc ccccgctgcc acacagccag 18

gctgaccagt acgtcctcag ctgggaccag cagctcaacc tcgcctatgt gggcgccgtc 240
 cctcaccgcg gcatacagca ggtccggacc cactggctgc tggagcttgt caccaccag 300
 gggccaccgt gacggggcct gagctacaac ttcaccacc tggacgggta ctggacctt 360
 ctcagggaga accagctcct ccaggggtt gagctgatgg gcagcgccctc gggccacttc 420
 actgactttg aggacaagca gcaggtgttt gagtggaaag acttggtctc cagcctggcc 480
 aggagatata tcggtaggtta cggactggcg catgtttcca agtggaaact cgagacgtgg 540
 aatgagccag accaccagca ctttgacaac gtctccatga ccatgcaagg ctctctgaac 600
 tactacgatg cctgctcgga gggctctgcg gccgcacgac ccgccctgcg gctgggaggc 660
 cccggcgact ccttccacac ccaccgcga tccccgctga gctggggcct cctgcgccac 720
 tgccacgacg gtaccaactt ctctactggg gagggcgcg tgcggttgga ctacatctcc 780
 ctccacagga aggggtgcg cgctccatc tccatcctgg agcaggagaa ggtcgtcgcg 840
 cagcagatcc ggcagctcct ccccaagttc gcggacacc ccatttaca cgacgaggcg 900
 gaccgcctgg tgggctggct cctgccacag ccgtggaggg cggacgtgac ctacgcggcc 960
 atggtggtga aggtcatcgc gcagcatcag aacctgtac tggccaacac cactccgcgc 1020
 ttccccacg cgtctctgag caacgacaat gccttctga gctaccaccc gaccccttc 1080
 gcgcagcgca cgtccacgc gcgcttccg gtaacaaca cccgccgcgc gcacgtgcag 1140
 ctgttcgca agccggtgct cagggccatg gggctgctgg cgtgctgga tgaggagcag 1200
 ctctggcgcg aagtgtcgca ggcggggacc gtcttgaca gcaaccacac ggtgggcgtc 1260
 ctggccagcg ccacccgcc ccaggggccg gcgcagccct ggcgcgcgcg ggtgctgac 1320
 tacgcgagcg acgacacccg cgcgccccc aaccgcagcg tcgcggtgac cctgcggctg 1380
 cgcggggtgc cccccggccc gggcctggtc tacgtcacgc gctacctgga caacgggctc 1440
 tgcagcccg acggcagtg gcggcgctg ggccggcccg tcttcccac ggcagagcag 1500
 ttccggcgca tgcgcgcgc tgaggaccgc gtggccgcg gcgcccgccc cttaccgcgc 1560
 ggcgcgccgc tgacctgcg cccgcgctg cggctgcctg cgcttttctg ggtgcaagt 1620
 tgtgcgcgc ccgagaagcc gccggggcag gtaacgcggc tcgcgcgcct gccctgacc 1680
 caaggcgacg tgggtctggt ctgctcgat gaacacgtg gctccaagt cctgtggaca 1740
 tacgagatcc agttctctca ggacggtaag gcgtacacc cggtcagcag gaagccatcg 1800
 accttaacc tcttctggt cagcccagac acaggtgctg tctctggctc ctaccgagtt 1860
 cgagccctg actactggg ccgaccagg cccttctcg accctgtgcc gtacctggag 1920
 gtccctgtgc caagagggcc cccatccccc ggcaatccat ga 1962

<210> 66
 <211> 653
 <212> PRT
 <213> Homo sapiens

 <400> 66
 Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
 1 5 10 15

 Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
 20 25 30

 Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
 35 40 45

 Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
 50 55 60

 Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
 65 70 75 80

 Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
 85 90 95

 Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
 100 105 110

 His Leu Asp Gly Tyr Leu Asp Leu Arg Glu Asn Gln Leu Leu Pro
 115 120 125

 Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
 130 135 140

 Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
 145 150 155 160

 Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
 165 170 175

 Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
 180 185 190

 Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
 195 200 205

 Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
 210 215 220

 Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
 225 230 235 240

 Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
 245 250 255

 Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
 260 265 270

 Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
 275 280 285

 Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val

290	295	300
Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala 305 310 315 320		
Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn 325 330 335		
Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe 340 345 350		
Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg 355 360 365		
Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys 370 375 380		
Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln 385 390 395 400		
Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His 405 410 415		
Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp 420 425 430		
Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala 435 440 445		
His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro 450 455 460		
Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu 465 470 475 480		
Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro 485 490 495		
Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala 500 505 510		
Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro 515 520 525		
Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro 530 535 540		
Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr 545 550 555 560		
Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys 565 570 575		
Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr 580 585 590		
Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser 595 600 605		
Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp 610 615 620		

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
645 650

<210> 67
<211> 1290
<212> DNA
<213> Homo sapiens

<400> 67
atgcagctga ggaaccaga actacatctg ggctgogcgc ttgcgcttcg cttcctggcc 60
ctcgtttcct gggacatccc tggggctaga gcactggaca atggattggc aaggacgcct 120
accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgccca ggaagagcca 180
gattcctgca tcagtgagaa gctcttcctg gagatggcag agctcatggt ctcagaaggc 240
tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaga 300
gattcagaag gcagacttca ggcagaccct cagcgctttc ctcattggat togccagcta 360
gctaattatg ttacacagca aggaactgaag ctagggatgt atgcagatgt tggaaataaa 420
acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatccca gacctttgct 480
gactggggag tagatctgct aaaatttgat ggttgttact gtgacagttt ggaaaaattg 540
gcagatggtt ataagcacat gtccttgccc ctgaatagga ctggcagaag cattgtgtac 600
tctgtgagt ggcctcttta tatgtggccc ttcaaaagc ccaattatac agaaatccga 660
cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
agtatcttgg actggacatc tttaaccag gagagaattg ttgatgttgc tggaccaggg 780
ggttggaatg accagatat gttagtalt ggcaactttg gcctcagctg gaatcagcaa 840
gtaactcaga tggcctctg ggcctatcatg gctgctcctt tattcatgtc taatgacctc 900
cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960
caggacccct tgggcaagca agggtaccag cttagacagg gagacaactt tgaagtgtgg 1020
gaacgcacct tctcaggctt agcctgggct gtacgtatga taaaccggca ggagattggt 1080
ggacctcgct cttataccat cgcagttgct tccctgggta aaggagtggc ctgtaactct 1140
gcctgttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaattgact 1200
tcaaggttaa gaagtcacat aaatoccaca ggcactgttt tgcttcagct agaaaaatac 1260
atgcagatgt cattaataa cttacttta 1290

<210> 68
<211> 429
<212> PRT
<213> Homo sapiens

<400> 68
 Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
 1 5 10 15
 Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240
 Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
 245 250 255
 Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
 260 265 270
 Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
 275 280 285
 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300
 Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

Gln Asp Pro Leu Gln Lys Gln Gly Tyr Gln Leu Arg Gln Trp Ala Asp Asn
325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
405 410 415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
420 425

<210> 69
<211> 351
<212> DNA
<213> Homo sapiens

<400> 69
atggattact acagaaaata tgcagctatc tttctgggtc cattgtcgggt gtttctgcatt 60
gttctccatt cgcctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaaccca 120
ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca 180
tatcccactc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240
tccacttgct gtgtagctaa atcatataac agggctcacg taatgggggg ttccaagtg 300
gagaaccaca cggcgtgccca ctgcagttact tgttattatc acaaatctta a 351

<210> 70
<211> 116
<212> PRT
<213> Homo sapiens

<400> 70
Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1 5 10 15
Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
20 25 30
Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
35 40 45
Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
50 55 60
Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

115 120 T25
 Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro
 130 135 140
 Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
 145 150 155 160
 Pro Ile Leu Pro Gln
 165

<210> 73
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 73
 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 1 5 10 15
 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 20 25 30
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
 35 40 45
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
 50 55 60
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
 65 70 75 80
 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 85 90 95
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 100 105 110
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 115 120 125
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 130 135 140
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 145 150 155 160
 Cys Arg Thr Gly Asp
 165

<210> 74
 <211> 588
 <212> DNA
 <213> Homo sapiens

<400> 74
 atggccctcc tgttccctct actggcagcc ctagtgatga ccagctatag cctctgttga 60
 tctctgggct gtgactctgcc tcagaacctt ggctacttta gcaggaacac ctgtgtgctt 120
 ctgcacaaaa tgaggagaat ctcccctttc ttgtgtctca aggacagaag agacttcagg 180

```

ttccccagg agatggtaaa agggagccag ttgcagaagg cccatgtcat gtctgtcctc 240
catgagatgc tgcagcagat cttcagcctc ttccacacag agcgtcctc tgctgcctgg 300
aacatgaccc tcttagacca actccacact ggacttcctc agcaactgca acacctggag 360
acctgcttgc tgcaggtagt gggagaagga gaatctgctg gggcaattag cagccctgca 420
ctgaccttga ggaggtactt ccagggaatc cgtgtctacc tgaagagaa gaaatacagc 480
gactgtgcct gggaagtgtt cagaatggaa atcatgaaat ccttgttctt atcaacaac 540
atgcaagaaa gactgagaag taaagataga gacctgggct catcttga 588

```

```

<210> 75
<211> 195
<212> PRT
<213> Homo sapiens

```

```

<400> 75
Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190

Gly Ser Ser
195

```